

GenCore version 5.1.6  
Copyright (c) 1993 - 2004 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: November 19, 2004, 23:28:53 ; Search time 15.9718 Seconds  
(without alignments)  
202.141 Million cell updates/sec

Title: US-10-068-725-4\_COPY\_110\_118  
Perfect score: 48  
Sequence: 1 SPVNLPPLE 9

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 2002273 seqs, 359729299 residues

Total number of hits satisfying chosen parameters: 2002273

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : A\_Geneseq\_23Sep04:\*

- 1: Geneseqp1980s:\*
- 2: Geneseqp1990s:\*
- 3: Geneseqp2000s:\*
- 4: Geneseqp2001s:\*
- 5: Geneseqp2002s:\*
- 6: Geneseqp2003as:\*
- 7: Geneseqp2003bs:\*
- 8: Geneseqp2004s:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Score | Query Match | Length | DB ID    | Description        |
|------------|-------|-------------|--------|----------|--------------------|
| 1          | 48    | 100.0       | 57     | AAU10953 | Aau10953 Human AGP |
| 2          | 48    | 100.0       | 166    | AAW75785 | Aaw75785 Human Lym |
| 3          | 48    | 100.0       | 166    | AAE15494 | Aae15494 Human TAC |
| 4          | 48    | 100.0       | 246    | ABP97720 | Abp97720 Amino aci |
| 5          | 48    | 100.0       | 246    | ADK00762 | Adk00762 Native hu |
| 6          | 48    | 100.0       | 247    | AAI93398 | Aay93398 Human BR4 |
| 7          | 48    | 100.0       | 247    | ABR61797 | Abt61797 Human RYZ |
| 8          | 48    | 100.0       | 265    | AAE09244 | Aae09244 Human TAC |
| 9          | 48    | 100.0       | 266    | ABP97723 | Abp97723 Amino aci |
| 10         | 48    | 100.0       | 291    | AAU10949 | Aau10949 Human AGP |
| 11         | 48    | 100.0       | 293    | AAW75783 | Aaw75783 Human Lym |
| 12         | 48    | 100.0       | 293    | AAE36312 | Aab36312 Human neu |
| 13         | 48    | 100.0       | 293    | AAI94000 | Aay94000 A transme |
| 14         | 48    | 100.0       | 293    | AAE09240 | Aae09240 Human TAC |
| 15         | 48    | 100.0       | 293    | AAV71914 | Aay71914 Human tra |
| 16         | 48    | 100.0       | 293    | AAO14130 | Aao14130 Human tra |
| 17         | 48    | 100.0       | 293    | ABB81488 | Abb81488 Human TAC |
| 18         | 48    | 100.0       | 293    | AAU99512 | Aau99512 Human TAC |
| 19         | 48    | 100.0       | 293    | AAE28962 | Aae28962 Human TAC |
| 20         | 48    | 100.0       | 293    | AAU75408 | Aau75408 Tumour ne |
| 21         | 48    | 100.0       | 293    | AAU09900 | Aau09900 Human AGP |
| 22         | 48    | 100.0       | 293    | AAE15493 | Aae15493 Human tra |
| 23         | 48    | 100.0       | 293    | ABG71496 | Abg71496 Human tum |
| 24         | 48    | 100.0       | 293    | AAE35211 | Aae35211 Human TAC |
| 25         | 48    | 100.0       | 293    | ABP60551 | Abp60551 Human tum |

|    |    |       |     |   |          |                    |
|----|----|-------|-----|---|----------|--------------------|
| 26 | 48 | 100.0 | 293 | 6 | ABP97716 | Abp97716 Amino aci |
| 27 | 48 | 100.0 | 293 | 6 | AAQ29592 | Aao29592 Human DIT |
| 28 | 48 | 100.0 | 293 | 7 | ADF72628 | Adf72628 Human tum |
| 29 | 48 | 100.0 | 293 | 7 | ADF77379 | Adf77379 Human tum |
| 30 | 48 | 100.0 | 293 | 8 | ADK00754 | Adk00754 Native hu |
| 31 | 48 | 100.0 | 293 | 8 | ADJ92514 | Adj92514 Human TAC |
| 32 | 48 | 100.0 | 293 | 8 | ADN03174 | Adn03174 Human TAC |
| 33 | 48 | 100.0 | 294 | 8 | ADK00765 | Adk00765 hTACI epl |
| 34 | 48 | 100.0 | 312 | 5 | AAO14135 | Aao14135 Protein o |
| 35 | 48 | 100.0 | 357 | 6 | AAE35226 | Aae35226 Human TAC |
| 36 | 48 | 100.0 | 392 | 6 | AAE35223 | Aae35223 Human TAC |
| 37 | 48 | 100.0 | 397 | 5 | AAE15498 | Aae15498 Human TAC |
| 38 | 48 | 100.0 | 404 | 5 | AAO14136 | Aao14136 Protein o |
| 39 | 40 | 83.3  | 780 | 2 | AAW11819 | Aaw11819 Candida a |
| 40 | 40 | 83.3  | 821 | 2 | AAW16611 | Aaw16611 Candida a |
| 41 | 39 | 81.2  | 905 | 5 | ABG93053 | Abg93053 S. cerevi |
| 42 | 39 | 81.2  | 905 | 6 | ABF53130 | Abf53130 Protein s |
| 43 | 39 | 81.2  | 905 | 7 | ADK62564 | Adk62564 Disease c |
| 44 | 38 | 79.2  | 84  | 4 | AAU58271 | Aau58271 Propionib |
| 45 | 38 | 79.2  | 84  | 6 | ABM54790 | Abm54790 Propionib |

ALIGNMENTS

RESULT 1

AAU10953  
ID AAU10953 standard; protein; 57 AA.  
XX  
AC AAU10953;  
XX  
DT 12-MAR-2002 (first entry)  
XX  
DE Human AGP-3 receptor stalk region.  
XX  
KW Human; AGP-3; antiinflammatory; antiarthritic; immunosuppressive;  
KW dermatological; neuroprotective; nootropic; immunomodulator; metabolic;  
KW antidiabetic; analgesic; nephrotropic; osteopathic; cytostatic; fever;  
KW antiparkinsonian; antipsoriatic; vasotropic; antibacterial; asthma;  
KW AGP-3 receptor; tumour necrosis factor ligand family; AGP-3 receptor;  
KW mesenteric lymph node; AGP-3R; inflammatory disease; immune disorder;  
KW rheumatoid arthritis; graft-versus-host disease; Crohn's disease;  
KW pancreatitis; amyotrophic lateral sclerosis; ALS; Alzheimer's disease;  
KW diabetes; glomerulonephritis; inflammatory bowel disease; ischaemia;  
KW multiple sclerosis; Parkinson's disease; transgenic animal.  
XX  
OS Homo sapiens.  
XX  
PN WO200185782-A2.  
XX  
PD 15-NOV-2001.  
XX  
PF 12-FEB-2001; 2001WO-US004568.  
XX  
PR 11-FEB-2000; 2000US-0181800P.  
XX  
PA (AMGE-) AMGEN INC.  
XX  
PI Boyle WJ, Hsu H;  
XX  
WI WPI; 2002-049441/06.  
XX  
PT Composition useful for identifying modulator of receptor for treating  
PT asthma and glomerulonephritis, comprises AGP-3 (tumour necrosis factor  
PT ligand family member) receptor and encoding nucleic acids.  
XX  
PS Disclosure; Fig 18; 124pp; English.  
XX  
CC The invention relates to a composition (I) comprising AGP-3 receptor  
CC (tumour necrosis factor ligand family member) related protein (II)  
CC attached to a vehicle protein. (I) is useful for modulating AGP-3-related  
CC activity in mesenteric lymph nodes (MLN) of a mammal. (II) is useful in  
CC assays to identify cells and tissues that express AGP-3R or proteins

CC related to AGP-3R-related protein and for identifying compounds (agonists  
 CC or antagonists) that interact with AGP-3R proteins. (II) is also useful  
 CC for identifying intracellular proteins that interact with the respective  
 CC cytoplasmic domains by yeast two-hybrid screening process. (II) is  
 CC involved in B cell growth, survival and activation particularly in lymph  
 CC node, spleen, and Peyer's patches. AGP-3R agonists and antagonists  
 CC identified using (II) are used for modulating B cell response and are  
 CC used to treat diseases characterised by inflammatory processes or  
 CC deregulated immune response such as rheumatoid arthritis, graft-versus-  
 CC host disease, Crohn's disease, lupus, etc. (II) is also useful in the  
 CC production of hybridoma cells which are derived from B cells, which  
 CC involves treating the hybridoma cells with (II). (II) is useful in the  
 CC treatment of inflammatory conditions of joints, e.g., rheumatoid  
 CC arthritis, osteoarthritis, etc. (II), its agonists or antagonists are  
 CC useful for treating acute pancreatitis, ankyroscopic lateral sclerosis  
 CC (ALS), Alzheimer's disease, asthma, atherosclerosis, cachexia/anorexia,  
 CC diabetes, fever, glomerulonephritis, inflammatory bowel disease,  
 CC ischaemic injury including cerebral ischaemia, multiple myeloma, multiple  
 CC sclerosis, osteoporosis, Parkinson's disease, pain, reperfusion injury,  
 CC septic shock, etc. The nucleic acids are also useful for developing the  
 CC transgenic animals expressing (II), which are useful for producing the  
 CC polypeptides and for the study of in vivo biological activity. The  
 CC present sequence represents the amino acid sequence of human AGP-3  
 CC receptor stalk region #1  
 XX  
 SQ Sequence 57 AA;

Query Match 100.0%; Score 48; DB 5; Length 57;  
 Best Local Similarity 100.0%; Pred. No. 1.7;  
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SPVNLPPPEL 9  
 DB 3 SPVNLPPPEL 11  
 |||||

RESULT 2  
 AAW75785  
 ID AAW75785 standard; protein; 166 AA.

XX AAW75785;

XX 18-JAN-1999 (first entry)

XX Human lymphocyte surface receptor extracellular domain.

XX TAC1; transmembrane activator and CAML-interactor;  
 XX calcium signal-modulating cyclophilin ligand; human;  
 XX lymphocyte surface receptor; human; B-cell; B lymphocyte; infection;  
 XX cancer; rheumatoid arthritis; autoimmune disease; glomerulonephritis;  
 XX immunosuppressive; graft versus host disease; transplant rejection;  
 XX therapy; signal transduction.

XX Homo sapiens.

XX WO9839361-A1.

XX 11-SEP-1998.

XX 03-MAR-1998; 98WO-US004270.

XX 03-MAR-1997; 97US-00810572.

XX (SJUD-) ST JUDE CHILDREN'S RES HOSPITAL.

XX Bram RJ, Von Bulow G;

XX WPI: 1998-506346/43.

XX N-PSDB; AAV57330.

XX New isolated transmembrane activator protein - used to develop products  
 XX for treating e.g. infections, cancers, autoimmune and inflammatory  
 XX conditions, transplant rejection or graft-versus-host disease.

XX Claim 8; Page 73; 89pp; English.

XX This is the amino acid sequence of the N-terminal, i.e. the  
 CC extracellular, domain of novel human transmembrane activator and CAML-  
 CC interactor (TAC1) protein (see AAW75783). TAC1 is a lymphocyte receptor  
 CC protein that is involved in the calcium activation pathway. It is  
 CC normally present in B-lymphocytes, and to a much lesser extent in  
 CC immature T-lymphocytes, and can therefore be targeted to specifically  
 CC regulate B cell responses without affecting T cell activity. The  
 CC extracellular domain of TAC1 functions as a binding site for a ligand  
 CC that stimulates the activation of the cell by inducing the binding of the  
 CC C-terminal portion (see AAW75784) of TAC1 to the N-terminal domain of  
 CC CAML. A recombinant form of the extracellular portion of TAC1 acts as a  
 CC dominant-negative or blocking agent and acts to suppress the immune  
 CC system. It can be used to treat or prevent autoimmune disease, graft  
 CC rejection or graft versus host disease. The extracellular region is also  
 CC used in a claimed method for identifying a ligand for TAC1, in which  
 CC binding of a candidate molecule is determined by detecting cellular  
 CC activation of the AP-1, CAMP or NF-KB pathway, of NF-AT transcription  
 CC factor, or of NF-AT dependent transcription  
 XX

SQ Sequence 166 AA;

Query Match 100.0%; Score 48; DB 2; Length 166;  
 Best Local Similarity 100.0%; Pred. No. 5.1;  
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SPVNLPPPEL 9  
 DB 110 SPVNLPPPEL 118  
 |||||

RESULT 3  
 AAE15494  
 ID AAE15494 standard; protein; 166 AA.

XX AAE15494;

XX 12-MAR-2002 (first entry)

XX Human TAC1 extracellular domain.

XX Human; transmembrane activator and intracellular CAML interactor; TAC1;  
 XX cytosolic; B cell maturation protein; BCMA; tumour necrosis factor; TNF;  
 XX lymphoproliferative disorder; tumour; lung; gastrointestinal; pancreatic;  
 XX prostate; inflammation; immune disorder; diarrhoea; psoriasis; colitis;  
 XX drug allergy; dermatitis; pneumonia; asthma; inflammatory bowel disease;  
 XX Crohn's disease; scleroderma; autoimmune disease; multiple sclerosis;  
 XX human immunodeficiency virus; HIV; systemic lupus erythematosus; cancer;  
 XX rheumatoid arthritis; atherosclerosis.

XX Homo sapiens.

XX WO200187979-A2.

XX 22-NOV-2001.

XX 14-MAY-2001; 2001WO-US015567.

XX 12-MAY-2000; 2000US-0204039P.

XX 27-JUN-2000; 2000US-0214591P.

XX 14-MAY-2001; 2001US-00214591.

XX (AMGE-) AMGEN INC.

XX Theill LE, Yu G;

XX WPI: 2002-066686/09.

XX Inhibiting activity of B cell maturation protein and/or transmembrane  
 XX activator and intracellular cyclophilin ligand interactor, by  
 XX administering a binding partner for APRIL, a tumor necrosis factor family

PT ligand.  
 XX Claim 1; Fig 12A; 94pp; English.  
 XX  
 CC The invention relates to a method for inhibiting TAC1 (transmembrane  
 CC activator and intracellular CAML interactor) and/or B cell maturation  
 CC protein (BCMA) activity in a mammal. The method comprises administering a  
 CC specific binding partner for APRIL (G70, a tumour necrosis factor-TNF  
 CC family ligand), having the consensus region of TAC1, BCMA, or the TAC1/  
 CC BCMA extracellular consensus sequence, but not the extracellular region  
 CC of TAC1 or BCMA. The method is useful for inhibiting activity of TAC1  
 CC and/or BCMA in a mammal which is useful for treating B-cell or T-cell  
 CC lymphoproliferative disorders, one or more solid tumours such as lung,  
 CC gastrointestinal, pancreatic or prostate tumour. APRIL, BCMA and TAC1  
 CC antagonists are useful for treating inflammation and immune function  
 CC diseases such as diarrhoea, psoriasis, allergies, pneumonia, atopic  
 CC dermatitis, respiratory allergic disease (asthma, hypersensitivity lung  
 CC disease), drug and insect sting allergy, inflammatory bowel disease  
 CC (Crohn's disease, colitis), scleroderma, autoimmune disease (multiple  
 CC sclerosis, rheumatoid arthritis, systemic lupus erythematosus), fungal,  
 CC bacterial, protozoal and viral infections (HIV), atherosclerosis, cancer  
 CC with leucocyte infiltration of the skin or organs. The present sequence  
 CC is human TAC1 protein extracellular domain  
 XX  
 XX Sequence 166 AA;  
 SQ

Query Match 100.0%; Score 48; DB 5; Length 166;  
 Best Local Similarity 100.0%; Pred. No. 5.1;  
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SPVNLPPPEL 9  
 |||||  
 Db 110 SPVNLPPPEL 118

RESULT 4  
 ABP97720  
 ID ABP97720 standard; protein; 246 AA.  
 AC ABP97720;  
 XX  
 DT 28-MAY-2003 (first entry)  
 DE Amino acid sequence of human TAC1 receptor.  
 XX  
 KW Human; TAC1; BR3; receptor; tumour necrosis factor ligand; TNF ligand;  
 KW TALL-1; April; systemic lupus erythematosus.  
 XX  
 OS Homo sapiens.  
 XX  
 PN WO2003014294-A2.  
 XX  
 PD 20-FEB-2003.  
 XX  
 PF 24-JUL-2002; 2002WO-US023487.  
 XX  
 PR 03-AUG-2001; 2001US-0310114P.  
 PR 30-APR-2002; 2002US-0377171P.  
 XX  
 XX (GETH ) GENENTECH INC.  
 PA  
 PI Dixit V, Grewal I, Ridgway J, Yan M;  
 XX  
 DR WPI: 2003-256560/25.  
 DR N-PSDB; ABZ68874.  
 XX  
 XX New nucleic acid encoding a TAC1s or BR3 polypeptide, useful for  
 PT preparing a composition for treating systemic lupus erythematosus.  
 XX  
 PS Disclosure; Fig 5B; 153pp; English.  
 XX

The present sequence represents a human TAC1 polypeptide. The  
 CC specification also describes BR3 polypeptides. TAC1 and BR3 are

CC receptors. Tumour necrosis factor (TNF) family ligands TALL-1 and April  
 CC bind to the TAC1 receptor, while TNF family ligands TALL-1 also binds to  
 CC BR3 receptor. The TAC1 and BR3 receptor nucleic acid is useful for  
 CC preparing a composition for treating systemic lupus erythematosus  
 XX  
 XX Sequence 246 AA;  
 SQ

Query Match 100.0%; Score 48; DB 6; Length 246;  
 Best Local Similarity 100.0%; Pred. No. 7.5;  
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SPVNLPPPEL 9  
 |||||  
 Db 64 SPVNLPPPEL 72

RESULT 5  
 ADK00762  
 ID ADK00762 standard; protein; 246 AA.  
 XX  
 AC ADK00762;  
 XX  
 DT 06-MAY-2004 (first entry)  
 DE Native human TAC1s.  
 XX  
 KW CAML interactor receptor; TAC1; Cytostatic; Antiinflammatory;  
 KW Dermatological; Immunosuppressive; Antirheumatic; Antiarthritic;  
 KW Antidiabetic; Neuroprotective; Antiasthmatic; Antiallergic; Anti-HIV;  
 KW Antibacterial; antiparasitic; systemic lupus erythematosus;  
 KW diabetes mellitus; AIDS.  
 XX  
 OS Homo sapiens.  
 XX  
 PN WO2004011611-A2.  
 XX  
 PD 05-FEB-2004.  
 XX  
 PF 25-JUL-2003; 2003WO-US023421.  
 XX  
 PR 25-JUL-2002; 2002US-0398530P.  
 XX  
 XX (GETH ) GENENTECH INC.  
 PA  
 PI Chuntharapai A, Grewal I, Kim KJ, Yan M;  
 XX  
 DR WPI: 2004-143841/14.  
 DR N-PSDB; ADK00761.  
 XX  
 XX New anti-TAC1 receptor monoclonal antibody, useful for diagnosing and  
 PT treating pathological conditions associated with tumor necrosis factor,  
 PT e.g. cancer or immune-related disease, such as rheumatoid arthritis or  
 PT psoriasis.  
 XX  
 PS Disclosure; SEQ ID NO 14; 110pp; English.  
 XX

The present invention relates to an isolated monoclonal antibody which  
 CC binds to a transmembrane activator of and CAML interactor (TAC1)  
 CC receptor. The TAC1 antibodies are useful for modulating TALL-1 or TAC1  
 CC polypeptide biological activity in mammalian cells, or for diagnosing and  
 CC treating pathological conditions associated with TNF and TNF receptor-  
 CC related molecules, e.g. cancer or immune-related disease, such as  
 CC systemic lupus erythematosus, rheumatoid arthritis, Sjogren's syndrome,  
 CC systemic vasculitis, diabetes mellitus, Crohn's disease,  
 CC glomerulonephritis, multiple sclerosis, psoriasis, asthma, urticaria or  
 CC infectious diseases including AIDS, hepatitis infection, bacterial  
 CC infection, fungal infection, protozoal infection and parasitic infection.  
 CC The present sequence represents native human TAC1s.  
 XX  
 XX Sequence 246 AA;  
 SQ

Query Match 100.0%; Score 48; DB 8; Length 246;  
 Best Local Similarity 100.0%; Pred. No. 7.5;

Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SPVNLPPPEL 9  
 Db 64 SPVNLPPPEL 72

RESULT 6  
 ID AAY93998 standard; protein; 247 AA.  
 XX AAY93998;  
 AC AAY93998;  
 DT 20-OCT-2000 (first entry)  
 DE Human BR43x2, an isoform of the TACI receptor.  
 XX Human; BR43x2; TACI receptor; extracellular domain; BCMA; B cell protein;  
 KW transmembrane activator and CAML-interactor; tumour necrosis factor; TNF;  
 KW ztnf4 activity; antibody production; autoimmune disease; amyloidosis;  
 KW systemic lupus erythematosus; myasthenia gravis; multiple sclerosis;  
 KW rheumatoid arthritis; asthma; bronchitis; emphysema; pyelonephritis;  
 KW end stage renal failure; glomerulonephritis; vasculitis; nephritis;  
 KW renal neoplasm; multiple myeloma; lymphoma; light chain neuropathy;  
 KW immune response; immunosuppression; graft rejection; joint pain;  
 KW graft versus host disease; inflammation; swelling; anaemia; septic shock;  
 KW insulin dependent diabetes mellitus; Crohn's disease; hypertension;  
 KW renal artery stenosis; occlusion; cholesterol; renal emboli.  
 XX Homo sapiens.  
 OS  
 XX  
 XX Key Location/Qualifiers  
 FH Domain 1..120  
 FT /note= "extracellular domain"  
 FT Region 25..58  
 FT /note= "cysteine-rich pseudo repeat"  
 FT Domain 121..133  
 FT /note= "transmembrane domain"  
 FT Domain 134..247  
 FT /note= "cytoplasmic domain"  
 XX  
 XX WO200040716-A2.  
 XX  
 XX 13-JUL-2000.  
 XX  
 XX 07-JAN-2000; 2000WO-US000396.  
 XX  
 XX 07-JAN-1999; 99US-00226533.  
 XX  
 XX (ZYMO ) ZYMOGENETICS INC.  
 XX  
 XX Gross JA, Xu W, Madden K, Yee DP;  
 XX WPI; 2000-452538/39.  
 XX N-PSDB; AAA58556.  
 XX  
 XX Inhibiting ztnf4 activity in a mammal, to treat autoimmune diseases,  
 XX renal disease, graft versus host disease, and inflammation, comprises  
 XX administering a BR43x2, TACI or BCMA extracellular domain polypeptide.  
 XX  
 XX Claim 62; Page 145; 175pp; English.  
 XX  
 XX The present sequence represents a human BR43x2 polypeptide, which is an  
 XX isoform of the transmembrane activator and CAML-interactor (TACI)  
 XX receptor. TACI is a tumour necrosis factor (TNF) receptor. The  
 XX extracellular domains of BR43x2, TACI or BCMA (a related B cell protein)  
 XX contain a cysteine rich domain, and are used for inhibiting ztnf4  
 XX activity. Ztnf4 is a TNF ligand. They may also be used for inhibiting  
 XX BR43x2, TACI or BCMA receptor-ligand engagement associated with activated  
 XX B lymphocytes, effector T-cells or with antibody production.  
 XX The antibody production is associated with an autoimmune disease selected  
 XX from systemic lupus erythematosus, myasthenia gravis, multiple sclerosis  
 XX and rheumatoid arthritis. The ztnf4 activity and BR43x2, TACI or BCMA

CC receptor-ligand engagement is associated with asthma, bronchitis,  
 CC emphysema, end stage renal failure, glomerulonephritis, vasculitis,  
 CC nephritis, pyelonephritis, renal neoplasms, multiple myelomas, lymphomas,  
 CC light chain neuropathy, amyloidosis, moderating immune response,  
 CC immunosuppression, graft rejection, Crohn's disease, joint  
 CC inflammation, insulin dependent diabetes mellitus, Crohn's disease, joint  
 CC pain, swelling, anaemia, or septic shock. BR43x2, TACI, and BCMA  
 CC polypeptides, fusions, antibodies, agonists or antagonists can be used to  
 CC treat hypertension, renal artery stenosis, or occlusion, and cholesterol  
 CC or renal emboli  
 XX  
 XX Sequence 247 AA;  
 SQ

Query Match 100.0%; Score 48; DB 3; Length 247;  
 Best Local Similarity 100.0%; Pred. No. 7.6;  
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SPVNLPPPEL 9  
 Db 64 SPVNLPPPEL 72

RESULT 7  
 ABR61797  
 ID ABR61797 standard; protein; 247 AA.  
 XX ABR61797;  
 AC ABR61797;  
 XX 12-SEP-2003 (first entry)  
 DT Human RYZN polypeptide.  
 DE  
 XX RYZN; TNFRSF; tumour necrosis factor receptor; antiarteriosclerotic;  
 KW type III transmembrane protein; antidiabetic; hypotensive; antilipemic;  
 KW human.  
 XX Homo sapiens.  
 OS  
 XX  
 XX Key Location/Qualifiers  
 FH Domain 1..113  
 FT /note= "extracellular domain"  
 FT Domain 114..136  
 FT /note= "transmembrane domain"  
 FT Domain 137..247  
 FT /note= "intracellular domain"  
 XX  
 XX WO2003045421-A1.  
 XX  
 XX 05-JUN-2003.  
 XX  
 XX 03-OCT-2002; 2002WO-IB004581.  
 XX  
 XX 28-NOV-2001; 2001US-0334152P.  
 XX  
 XX (GEST ) GENSET SA.  
 XX  
 XX Djalynas D, Scallia A, Lucas J, Briggs K;  
 XX WPI; 2003-513616/48.  
 XX N-PSDB; ACC84638.  
 XX  
 XX New agonists or antagonists of RYZN activity, useful for increasing or  
 XX reducing body weight, for maintaining weight loss, and for preventing or  
 XX treating an obesity-related disease or disorder, e.g. atherosclerosis or  
 XX diabetes.  
 XX  
 XX Example; Page 32-33; 37pp; English.  
 XX  
 XX The invention relates to an agonist or antagonist of RYZN activity. RYZN  
 XX is a member of the Tumour Necrosis Factor Receptor Super Family (TNFRSF)  
 XX and is a type III transmembrane protein. The agonist or antagonist of  
 XX RYZN activity, or compositions comprising them is useful for preventing  
 XX or treating an obesity-related disease or disorder, such as insulin

CC resistance, hyperlipidemia, atherosclerosis, diabetes, hypertension, syndrome X, and hyperuricemia. These may also be used to increase or reduce body weight, or maintain weight loss. The present sequence represents the human RYZN polypeptide

XX SQ Sequence 247 AA;

Query Match 100.0%; Score 48; DB 7; Length 247;  
Best Local Similarity 100.0%; Pred. No. 7.6;  
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SPVNLPPPEL 9  
Db 64 SPVNLPPPEL 72  
|||||

RESULT 8  
AAE09244  
ID AAE09244 standard; protein; 265 AA.

XX AAE09244;

DT 19-NOV-2001 (first entry)

DE Human TACI splice variant protein.

KW Human; TNF; tumour necrosis factor; TALL-1; APRIL; TNF receptor; TNFR;  
KW TACI; BCMA; therapy; cancer; leukaemia; myeloma; lymphoma;  
KW autoimmune disease; rheumatoid arthritis; multiple sclerosis; psoriasis.

XX OS Homo sapiens.

XX PN WO200160397-A1.

XX PD 23-AUG-2001.

XX PF 28-NOV-2000; 2000WO-US032378.

XX PR 16-FEB-2000; 2000US-0182938P.

XX PR 22-AUG-2000; 2000US-0226986P.

XX PA (GETH ) GENENTECH INC.

XX PI Ashkenazi AJ, Dodge KH, Grewal I, Kim KJ, Marsters SA, Pitti RM;  
XX PI Yan M;

XX DR WPI; 2001-541628/60.

XX PT Inhibiting or neutralizing TALL-1 or APRIL polypeptide biological activity, for treating autoimmune disorders and cancer, comprises exposing the cells to TALL-1 or APRIL polypeptide agonists or antagonists.

XX FS Example 1; Fig 6; 160pp; English.

XX CC The invention relates to methods of using one or more agonists or antagonists to modulate the activity of the members of TNF (tumour necrosis factor) especially TALL-1, APRIL and TNF receptor (TNFR) e.g. TACI or BCMA. The method is useful for treating pathological conditions or diseases associated with increased TALL-1 and APRIL expression or activity. TALL-1 and APRIL antagonists are used to block the interaction between APRIL and TALL-1 with TACI or BCMA. They are useful for treating a mammal suffering from cancer such as leukaemia, lymphoma, myeloma, cancers of lung and colon and autoimmune diseases e.g. rheumatoid arthritis, multiple sclerosis, psoriasis and lupus erythematosus. The present sequence is human TACI splice variant protein

XX SQ Sequence 265 AA;

Query Match 100.0%; Score 48; DB 4; Length 265;  
Best Local Similarity 100.0%; Pred. No. 8.1;  
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SPVNLPPPEL 9  
Db 110 SPVNLPPPEL 118  
|||||

RESULT 9

ID ABP97723 standard; protein; 266 AA.

XX AC ABP97723;

XX DT 28-MAY-2003 (first entry)

XX DE Amino acid sequence of an alternatively spliced human TACI receptor.  
XX KW Human; TACI; BR3; receptor; tumour necrosis factor ligand; TNF ligand;  
XX KW TALL-1; April; systemic lupus erythematosus.

XX OS Homo sapiens.

XX PN WO2003014294-A2.

XX PD 20-FEB-2003.

XX PF 24-JUL-2002; 2002WO-US023487.

XX PR 03-AUG-2001; 2001US-0310114P.

XX PR 30-APR-2002; 2002US-0377171P.

XX PA (GETH ) GENENTECH INC.

XX PI Dixit V, Grewal I, Ridgway J, Yan M;

XX DR WPI; 2003-256560/25.

XX PT New nucleic acid encoding a TACIs or BR3 polypeptide, useful for preparing a composition for treating systemic lupus erythematosus.

XX PS Disclosure; Fig 8; 153pp; English.

XX CC The present sequence represents an alternatively spliced human TACI polypeptide. The specification also describes BR3 polypeptides. TACI and BR3 are receptors. Tumour necrosis factor (TNF) family ligands TALL-1 and April bind to the TACI receptor, while TNF family ligands TALL-1 also binds to BR3 receptor. The TACI and BR3 receptor nucleic acid is useful for preparing a composition for treating systemic lupus erythematosus

XX SQ Sequence 266 AA;

Query Match 100.0%; Score 48; DB 6; Length 266;

Best Local Similarity 100.0%; Pred. No. 8.1;

Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SPVNLPPPEL 9  
Db 110 SPVNLPPPEL 118  
|||||

RESULT 10

AAU10949

ID AAU10949 standard; protein; 291 AA.

XX AC AAU10949;

XX DT 12-MAR-2002 (first entry)

XX DE Human AGP-3 receptor extracellular domain.

XX KW Human; AGP-3; antiinflammatory; antiarthritic; immunosuppressive;  
XX KW dermatological; neuroprotective; nootropic; immunomodulator; metabolic;  
XX KW antidiabetic; analgesic; nephrotropic; osteopathic; cytostatic; fever;  
XX KW antiparkinsonian; antipsoriatic; vasotropic; antibacterial; asthma;  
XX KW AGP-3 receptor; tumour necrosis factor ligand family; AGP-3 receptor;

mesenteric lymph node; AGP-3R; inflammatory disease; immune disorder; rheumatoid arthritis; graft-versus-host disease; Crohn's disease; pancreatitis; amyotrophic lateral sclerosis; ALS; Alzheimer's disease; diabetes; glomerulonephritis; inflammatory bowel disease; ischaemia; multiple sclerosis; Parkinson's disease; transgenic animal.

Homo sapiens.

W0200185782-A2.

15-NOV-2001.

12-FEB-2001; 2001WO-US004568.

11-FEB-2000; 2000US-0181800P.

(AMGE-) AMGEN INC.

Boyle WJ, Hsu H;

WPI; 2002-049441/06.

Composition, useful for identifying modulator of receptor for treating asthma and glomerulonephritis, comprises AGP-3 (tumor necrosis factor ligand family member) receptor and encoding nucleic acids.

Claim 1; Fig 18; 12app; English.

The invention relates to a composition (I) comprising AGP-3 receptor (tumour necrosis factor ligand family member) related protein (II) attached to a vehicle protein. (I) is useful for modulating AGP-3-related activity in mesenteric lymph nodes (MLN) of a mammal. (II) is useful in assays to identify cells and tissues that express AGP-3R or proteins related to AGP-3R-related protein and for identifying compounds (agonists or antagonists) that interact with AGP-3R proteins. (II) is also useful for identifying intracellular proteins that interact with the respective cytoplasmic domains by yeast two-hybrid screening process. (II) is involved in B cell growth, survival and activation particularly in lymph node, spleen, and Peyer's patches. AGP-3R agonists and antagonists identified using (II) are used for modulating B cell response and are used to treat diseases characterised by inflammatory processes or deregulated immune response such as rheumatoid arthritis, graft-versus-host disease, Crohn's disease, lupus, etc. (II) is also useful in the production of hybridoma cells which are derived from B cells, which involves treating the hybridoma cells with (II). (II) is useful in the treatment of inflammatory conditions of joints, e.g., rheumatoid arthritis, osteoarthritis, etc. (II), its agonists or antagonists are useful for treating acute pancreatitis, amyotrophic lateral sclerosis (ALS), Alzheimer's disease, asthma, atherosclerosis, cachexia/anorexia, diabetes, fever, glomerulonephritis, inflammatory bowel disease, multiple myeloma, multiple sclerosis, osteoporosis, Parkinson's disease, pain, reperfusion injury, septic shock, etc. The nucleic acids are also useful for developing transgenic animals expressing (II), which are useful for producing the polypeptides and for the study of in vivo biological activity. The present sequence represents the amino acid sequence of human AGP-3 extracellular domain

Sequence 291 AA;

Query Match 100.0%; Score 48; DB 5; Length 291;  
Best Local Similarity 100.0%; Pred. No. 8.9;  
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SPVNLPEEL 9  
| | | | | | | | | |  
Db 110 SPVNLPEEL 118

RESULT 11  
AAW75783  
ID AAW75783 standard; protein; 293 AA.  
XX

AC AAW75783;  
XX 18-JAN-1999 (first entry)  
XX Human lymphocyte surface receptor TACI.  
DE  
XX  
XX TACI; transmembrane activator and CAML-interactor;  
KW calcium signal-modulating cyclophilin ligand; human;  
KW lymphocyte surface receptor; human; B-cell; B lymphocyte; infection;  
KW cancer; rheumatoid arthritis; autoimmune disease; glomerulonephritis;  
KW immunosuppressive; graft versus host disease; transplant rejection;  
KW therapy.  
XX  
XX Homo sapiens.  
OS  
XX  
XX Key Location/Qualifiers  
FH Domain 1. .166  
FT /label= Extracellular\_domain  
FT /note= "Claim 8"  
FT Peptide 34. .71  
FT /note= "TNFR NGPR motif"  
FT Domain 167. .186  
FT /label= Transmembrane\_domain  
FT Domain 187. .294  
FT /label= Cytoplasmic\_domain  
FT /note= "Claim 6"  
XX  
XX W098939361-A1.  
PN  
XX  
XX 11-SEP-1998.  
XX  
XX 03-MAR-1998; 98WO-US004270.  
XX  
XX 03-MAR-1997; 97US-00810572.  
XX (STUD-) ST JUDE CHILDREN'S RES HOSPITAL.  
XX  
XX Bram RJ, Von Bulow G;  
XX WPI; 1998-506346/43.  
XX N-PSDB; AAV57328.  
XX New isolated transmembrane activator protein - used to develop products for treating e.g. infections, cancers, autoimmune and inflammatory conditions, transplant rejection or graft-versus-host disease.  
XX Claim 20; Fig 2a; 89pp; English.  
XX This is the amino acid sequence of novel human transmembrane activator and CAML-interactor (TACI) protein, a lymphocyte receptor protein that is involved in the calcium activation pathway. TACI is normally present in B-lymphocytes, and to a much lesser extent in immature T-lymphocytes, and can therefore be targeted to specifically regulate B cell responses without affecting T cell activity. TACI cDNA (seeV57328) was isolated from a B-lymphocyte cDNA library using a yeast two-hybrid assay. Also claimed are the C-terminal (see AAW75784) and N-terminal (see AAW75785) fragments of TACI, recombinant DNA constructs, unicellular hosts, and antibodies to TACI protein. Methods are claimed for identifying a ligand for TACI and for identifying immunosuppressive drugs that selectively block the action of B lymphocytes without affecting mature T lymphocytes. TACI can be activated to increase immune system activity, e.g. for treating infections or cancers. It can be blocked to provide immunosuppression, e.g. for treating autoimmune and inflammatory conditions such as immune complex-induced vasculitis, glomerulonephritis, haemolytic anaemia, myasthenia gravis, type II collagen-induced arthritis, experimental allergic and hyperacute xenograft rejection, rheumatoid arthritis, systemic lupus erythematosus, transplant rejection, cancer or graft versus host disease  
XX Sequence 293 AA;  
SQ

Query Match 100.0%; Score 48; DB 2; Length 293;  
Best Local Similarity 100.0%; Pred. No. 9;

Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SPVNLPPPEL 9  
 |||||  
 Db 110 SPVNLPPPEL 118

## RESULT 12

AAB36312  
 ID AAB36312 standard; protein; 293 AA.

XX AC AAB36312;

DT 26-FEB-2001 (first entry)

XX Human neutrokinine-alpha binding protein TR17 SEQ ID NO:2.

XX Human; neutrokinine-alpha binding protein; NAR protein; TR17; cytostatic;  
 KW immunosuppressive; neutrotropic; neuroprotective; antiviral; antiallergic;  
 KW hepatotropic; antidiabetic; antiinflammatory; antiulcer; cardiant;  
 KW ophthalmological; gene therapy; immunodeficiency disorder; diagnosis;  
 KW autoimmune disorder.

XX OS Homo sapiens.

XX PN WO200059362-A1.

XX PD 05-OCT-2000.

XX PF 24-MAR-2000; 2000WO-US007966.

XX PR 26-MAR-1999; 99US-0126599P.

XX PR 10-MAR-2000; 2000US-0186208P.

XX PA (HUMA-) HUMAN GENOME SCI INC.

XX PI Ruben SM, Ullrich S, Baker K;

XX DR WPI; 2000-602359/57.

XX DR N-PSDB; AAC64602.

XX Nucleic acid encoding a neutrokinine-alpha receptor (NAR) such as TR17,  
 PT useful for producing TR17 protein which is used in the treatment and  
 PT diagnosis of autoimmune and immunodeficiency disorders.

XX Claim 1; Fig 1; 398pp; English.

XX The present sequence represents the human neutrokinine-alpha binding (NAR)  
 CC protein designated TR17. TR17 has cytostatic, immunosuppressive,  
 CC neutrotropic, neuroprotective, antiviral, antiallergic, hepatotropic,  
 CC antidiabetic, antiinflammatory, antiulcer, cardiant and ophthalmological  
 CC activities and can be used in gene therapy. The TR17 protein and  
 CC antibodies are useful for treating and diagnosing immunodeficiency  
 CC disorders and autoimmune disorders. The TR17 polypeptides,  
 CC polynucleotides, antibodies, agonists and/or antagonists are used for  
 CC treating various other diseases defined in the specification and as  
 CC research tools for studying the phenotypic effects that result from  
 CC inhibiting TR17/TR17 ligand interactions on various cell types

XX Sequence 293 AA;

Query Match 100.0%; Score 48; DB 3; Length 293;

Best Local Similarity 100.0%; Pred. No. 9;

Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SPVNLPPPEL 9  
 |||||  
 Db 110 SPVNLPPPEL 118

## RESULT 13

AAY94000  
 ID AAY94000 standard; protein; 293 AA.

XX

AC AAY94000;

DT 20-OCT-2000 (first entry)

DE A transmembrane activator and CAML-interactor (TACI).

XX Human; BR43x2; TACI receptor; extracellular domain; BCMA; B cell protein;  
 KW transmembrane activator and CAML-interactor; tumour necrosis factor; TNF;  
 KW ztnf4 activity; antibody production; autoimmune disease; amyloidosis;  
 KW systemic lupus erythematosus; myasthenia gravis; multiple sclerosis;  
 KW rheumatoid arthritis; asthma; bronchitis; emphysema; pyelonephritis;  
 KW end stage renal failure; glomerulonephritis; vasculitis; nephritis;  
 KW renal neoplasm; multiple myeloma; lymphoma; light chain neuropathy;  
 KW immune response; immunosuppression; graft rejection; joint pain;  
 KW graft versus host disease; inflammation; swelling; anaemia; septic shock;  
 KW insulin dependent diabetes mellitus; Crohn's disease; hypertension;  
 KW renal artery stenosis; occlusion; cholesterol; renal emboli.

XX OS Homo sapiens.

XX PN WO200040716-A2.

XX PD 13-JUL-2000.

XX PF 07-JAN-2000; 2000WO-US000396.

XX PR 07-JAN-1999; 99US-00226533.

XX PA (ZYMO) ZYMOGENETICS INC.

XX PI Gross JA, Xu W, Madden K, Yee DP;

XX WPI; 2000-452538/39.

XX DR N-PSDB; AAA58558.

XX Inhibiting ztnf4 activity in a mammal, to treat autoimmune diseases,  
 PT renal disease, graft versus host disease, and inflammation, comprises  
 PT administering a BR43x2, TACI or BCMA extracellular domain polypeptide.

XX Disclosure; Page 149-150; 175pp; English.

XX The present sequence represents a human transmembrane activator and CAML-  
 CC interactor (TACI) receptor. TACI is a tumour necrosis factor (TNF)  
 CC receptor. The extracellular domains of BR43x2 (an isoform of TACI), TACI  
 CC or BCMA (a related B cell protein) receptor contain a cysteine rich  
 CC domain, and are used for inhibiting ztnf4 activity. Ztnf4 is a TNF  
 CC ligand. They may also be used for inhibiting BR43x2, TACI or BCMA  
 CC receptor-ligand engagement associated with activated or resting B  
 CC lymphocytes, effector T-cells, or with antibody production. The antibody  
 CC production is associated with an autoimmune disease selected from  
 CC systemic lupus erythematosus, myasthenia gravis, multiple sclerosis and  
 CC rheumatoid arthritis. The ztnf4 activity and BR43x2, TACI or BCMA  
 CC receptor-ligand engagement is associated with asthma, bronchitis,  
 CC emphysema, end stage renal failure, glomerulonephritis, vasculitis,  
 CC nephritis, pyelonephritis, renal neoplasms, multiple myelomas, lymphomas,  
 CC light chain neuropathy, amyloidosis, moderating immune response,  
 CC immunosuppression, graft rejection, graft versus host disease,  
 CC inflammation, insulin dependent diabetes mellitus, Crohn's disease, joint  
 CC pain, swelling, anaemia, or septic shock. BR43x2, TACI, and BCMA  
 CC polypeptides, fusions, antibodies, agonists or antagonists can be used to  
 CC treat hypertension, renal artery stenosis, or occlusion, and cholesterol  
 CC or renal emboli

XX Sequence 293 AA;

Query Match 100.0%; Score 48; DB 3; Length 293;

Best Local Similarity 100.0%; Pred. No. 9;

Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SPVNLPPPEL 9

Db 110 SPVNLPPPEL 118

RESULT 14  
AAE09240  
ID AAE09240 standard; protein; 293 AA.

AC AAE09240;  
DT 19-NOV-2001 (first entry)  
XX

DE Human TACI protein.

XX Human; TNF; tumour necrosis factor; TALL-1; APRIL; TNF receptor; TNFR;  
KW TACI; BCMA; therapy; cancer; leukaemia; myeloma; lymphoma;  
KW autoimmune disease; rheumatoid arthritis; multiple sclerosis; psoriasis.

OS Homo sapiens.

PN WO200160397-A1.

XX 23-AUG-2001.

XX 28-NOV-2000; 2000WO-US032378.

XX 16-FEB-2000; 2000US-0182938P.

XX 22-AUG-2000; 2000US-0236986P.

XX (GETH ) GENENTECH INC.

XX Ashkenazi AJ, Dodge KH, Grewal I, Kim KJ, Marsters SA, Pitti RM;  
PI Yan M;

DR WPI: 2001-541628/60.

DR N-PSDB; AAD15901.

XX Inhibiting or neutralizing TALL-1 or APRIL polypeptide biological  
PT activity, for treating autoimmune disorders and cancer, comprises  
PT exposing the cells to TALL-1 or APRIL polypeptide agonists or  
PT antagonists.

PS Example 1; Fig 1; 160pp; English.

XX The invention relates to methods of using one or more agonists or  
CC antagonists to modulate the activity of the members of TNF (tumour  
CC necrosis factor) especially TALL-1, APRIL and TNF receptor (TNFR) e.g.  
CC TACI or BCMA. The method is useful for treating pathological conditions  
CC or diseases associated with increased TALL-1 and APRIL expression or  
CC activity. TALL-1 and APRIL antagonists are used to block the interaction  
CC between APRIL and TALL-1 with TACI or BCMA. They are useful for treating  
CC a mammal suffering from cancer such as leukaemia, lymphoma, myeloma,  
CC cancers of lung and colon and autoimmune diseases e.g. rheumatoid  
CC arthritis, multiple sclerosis, psoriasis and lupus erythematosus. The  
CC present sequence is human TACI protein

XX Sequence 293 AA;

Query Match 100.0%; Score 48; DB 4; Length 293;  
Best Local Similarity 100.0%; Pred. No. 9;  
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SPVNLPPPEL 9  
Db 110 SPVNLPPPEL 118

RESULT 15

AAAY71914  
ID AAY71914 standard; protein; 293 AA.

AC AAY71914;

XX 26-MAR-2001 (first entry)

XX

DE Human tumour necrosis factor receptor (TACI) protein.

XX Human; transmembrane activator and CAML interactor; TACI;  
KW tumour necrosis factor receptor; TNF; autoimmune disease; diabetes;  
KW calcium-signal modulating cyclophilin ligand; CAML; viral infection;  
KW neutrokin alpha polypeptide; TACI-Ligand; TACI-L; cytostatic; therapy;  
KW neuroprotective; antidiabetic; antiviral; antiinflammatory; tumour;  
KW antiarthritic; antirheumatic; immunosuppressive; multiple sclerosis;  
KW rheumatoid arthritis; graft rejection; inflammation; cell proliferation;  
KW cell death; immunoglobulin E-mediated allergic reaction; IgE.

XX Homo sapiens.

XX Key Location/Qualifiers  
FH Domain 2..166

FT /label= Extracellular domain  
FT /note= "Binds with amino acids 123-285 of extracellular  
FT domain of TACI-L"

XX WO200067034-A1.

XX 09-NOV-2000.

XX 14-APR-2000; 2000WO-US010282.

XX 30-APR-1999; 99US-00302863.

XX (IMV ) IMMUNEX CORP.

XX Goodwin RG, Din WS;

XX WPI: 2001-016005/02.

XX N-PSDB; AAD02006.

XX Use of new interactions between tumor necrosis factor receptors (TACI)  
PT and TACI ligands to screen candidate molecules for determining agonist  
PT and antagonist interactions which are used for treating inflammation.

PS Claim 10; Fig 1b; 46pp; English.

XX The present sequence is a human tumour necrosis factor receptor (TACI)  
CC protein. TACI (Transmembrane activator and calcium-signal modulating  
CC cyclophilin ligand (CAML)-interactor) forms a complex with neutrokin  
CC alpha polypeptide (TACI-Ligand). The antagonist or agonist of TACI/TACI-L  
CC complex is useful for modulating an intracellular signalling cascade  
CC mediated by TACI/TACI-L complex. Antagonists of TACI/TACI-L complex are  
CC used to inhibit the interaction between TACI and TACI-L for therapeutic  
CC purposes to treat tumour and tumour metastasis and to combat various  
CC autoimmune diseases e.g. multiple sclerosis and diabetes, as well as  
CC other disorders, such as viral infection, rheumatoid arthritis, graft  
CC rejection, and immunoglobulin (Ig) E-mediated allergic reactions and  
CC inflammation. The interaction is used to study cellular processes  
CC associated with tumour necrosis factor (TNF)-receptors such as immune  
CC regulation, cell proliferation, cell death and inflammatory responses.  
CC The interaction between the extracellular region of TACI and TACI-L can  
CC be used to further develop understanding of which cell types TACI-L acts  
CC upon

XX Sequence 293 AA;

Query Match 100.0%; Score 48; DB 4; Length 293;  
Best Local Similarity 100.0%; Pred. No. 9;  
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SPVNLPPPEL 9  
Db 110 SPVNLPPPEL 118

Search completed: November 19, 2004, 23:40:03  
Job time : 16.9718 secs



GenCore version 5.1.6  
Copyright (c) 1993 - 2004 Compugen Ltd.

OM protein - protein search, using sw model

Run on: November 19, 2004, 23:37:09 ; Search time 7.09859 Seconds  
(without alignments)  
84.082 Million cell updates/sec

Title: US-10-068-725-4\_COPY\_110\_118  
Perfect score: 48  
Sequence: 1 SPVNPPEL 9

Scoring table: BLASTUM62  
Gapop 10.0 , Gapext 0.5

Searched: 478139 seqs, 66318000 residues

Total number of hits satisfying chosen parameters: 478139

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000  
Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : Issued Patents AA:\*  
1: /cgn2\_6/ptodata/1/1aa/5A-COMB.pep:\*  
2: /cgn2\_6/ptodata/1/1aa/5B-COMB.pep:\*  
3: /cgn2\_6/ptodata/1/1aa/6A-COMB.pep:\*  
4: /cgn2\_6/ptodata/1/1aa/6B-COMB.pep:\*  
5: /cgn2\_6/ptodata/1/1aa/PCTUS-COMB.pep:\*  
6: /cgn2\_6/ptodata/1/1aa/backfiles1.pep:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Score | Query Match | Length | ID | Description          |
|------------|-------|-------------|--------|----|----------------------|
| 1          | 48    | 100.0       | 166    | 2  | US-08-810-572A-6     |
| 2          | 48    | 100.0       | 166    | 3  | US-09-290-333-6      |
| 3          | 48    | 100.0       | 166    | 4  | US-09-782-857A-6     |
| 4          | 48    | 100.0       | 166    | 4  | US-09-854-864-15     |
| 5          | 48    | 100.0       | 293    | 2  | US-08-810-572A-2     |
| 6          | 48    | 100.0       | 293    | 3  | US-09-290-333-2      |
| 7          | 48    | 100.0       | 293    | 4  | US-09-782-857A-2     |
| 8          | 48    | 100.0       | 293    | 4  | US-09-879-919-22     |
| 9          | 48    | 100.0       | 293    | 4  | US-09-848-295-4      |
| 10         | 48    | 100.0       | 293    | 4  | US-09-854-864-14     |
| 11         | 48    | 100.0       | 397    | 4  | US-09-854-864-18     |
| 12         | 40    | 83.3        | 456    | 4  | US-09-248-796A-19216 |
| 13         | 40    | 83.3        | 780    | 1  | US-08-485-621-2      |
| 14         | 40    | 83.3        | 780    | 2  | US-08-973-831-2      |
| 15         | 40    | 83.3        | 780    | 5  | PCT-US96-09530A-2    |
| 16         | 38    | 79.2        | 458    | 4  | US-09-252-991A-22614 |
| 17         | 37    | 77.1        | 1093   | 4  | US-09-252-991A-21827 |
| 18         | 36    | 75.0        | 201    | 4  | US-09-252-991A-32333 |
| 19         | 36    | 75.0        | 211    | 4  | US-09-248-796A-22369 |
| 20         | 35    | 72.9        | 150    | 4  | US-09-513-999C-6406  |
| 21         | 35    | 72.9        | 162    | 4  | US-10-101-464A-526   |
| 22         | 35    | 72.9        | 642    | 4  | US-09-252-991A-27045 |
| 23         | 35    | 72.9        | 1164   | 3  | US-09-457-708-2      |
| 24         | 35    | 72.9        | 1164   | 4  | US-09-950-048A-2     |
| 25         | 35    | 72.9        | 1164   | 4  | US-09-976-594-989    |
| 26         | 34    | 70.8        | 268    | 3  | US-08-652-877-4      |
| 27         | 34    | 70.8        | 268    | 3  | US-08-476-515A-4     |

|    |    |      |      |   |                      |                   |
|----|----|------|------|---|----------------------|-------------------|
| 28 | 34 | 70.8 | 385  | 4 | US-09-489-039A-11265 | Sequence 11265, A |
| 29 | 34 | 70.8 | 434  | 4 | US-10-265-012-10     | Sequence 10, Appl |
| 30 | 34 | 70.8 | 569  | 4 | US-10-265-012-8      | Sequence 8, Appl  |
| 31 | 34 | 70.8 | 608  | 4 | US-10-265-012-2      | Sequence 2, Appl  |
| 32 | 34 | 70.8 | 943  | 3 | US-08-476-515A-12    | Sequence 12, Appl |
| 33 | 34 | 70.8 | 944  | 3 | US-08-652-877-12     | Sequence 12, Appl |
| 34 | 34 | 70.8 | 968  | 3 | US-09-302-812-6      | Sequence 6, Appl  |
| 35 | 34 | 70.8 | 968  | 3 | US-09-511-477-6      | Sequence 6, Appl  |
| 36 | 34 | 70.8 | 968  | 3 | US-09-511-507-6      | Sequence 6, Appl  |
| 37 | 34 | 70.8 | 4654 | 3 | US-08-476-515A-84    | Sequence 84, Appl |
| 38 | 34 | 70.8 | 4655 | 3 | US-08-652-877-84     | Sequence 84, Appl |
| 39 | 34 | 70.8 | 4655 | 3 | US-08-652-877-86     | Sequence 86, Appl |
| 40 | 34 | 70.8 | 4655 | 3 | US-08-652-877-88     | Sequence 88, Appl |
| 41 | 34 | 70.8 | 4655 | 3 | US-08-652-877-90     | Sequence 90, Appl |
| 42 | 33 | 68.8 | 22   | 4 | US-09-270-767-40902  | Sequence 40902, A |
| 43 | 33 | 68.8 | 22   | 4 | US-09-270-767-56118  | Sequence 56118, A |
| 44 | 33 | 68.8 | 75   | 4 | US-09-270-767-60082  | Sequence 60082, A |
| 45 | 33 | 68.8 | 148  | 4 | US-09-270-767-39112  | Sequence 39112, A |

ALIGNMENTS

RESULT 1  
US-08-810-572A-6  
; Sequence 6, Application US/08810572A  
; Patent No. 5969102  
; GENERAL INFORMATION:  
; APPLICANT: Bram, Richard J.  
; APPLICANT: von Bulow, Gotz  
; TITLE OF INVENTION: A LYMPHOCYTE SURFACE RECEPTOR THAT BINDS  
; TITLE OF INVENTION: CAML, NUCLEIC ACIDS ENCODING THE SAME AND METHODS OF USE  
; NUMBER OF SEQUENCES: 11  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: David A. Jackson, Esq.  
; STREET: 411 Hackensack Ave, Continental Plaza, 4th  
; STREET: Floor  
; CITY: Hackensack  
; STATE: New Jersey  
; COUNTRY: USA  
; ZIP: 07601  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/810,572A  
; FILING DATE: 28-FEB-1997  
; CLASSIFICATION: 536  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Jackson Esq., David A.  
; REGISTRATION NUMBER: 26,742  
; REFERENCE/DOCKET NUMBER: 1340-1-007  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 201-487-5800  
; TELEFAX: 201-343-1684  
; INFORMATION FOR SEQ ID NO: 6:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 166 amino acids  
; TYPE: amino acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: peptide  
; HYPOTHETICAL: NO  
; FRAGMENT TYPE: N-terminal  
; ORIGINAL SOURCE:  
; ORGANISM: Homo sapiens  
US-08-810-572A-6

Query Match 100.0%; Score 48; DB 2; Length 166;  
Best Local Similarity 100.0%; Pred. No. 0.7;

Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 SPVNLPEL 9  
Db 110 SPVNLPEL 118

## RESULT 2

US-09-290-333-6  
; Sequence 6, Application US/09290333  
; Patent No. 6316222  
; GENERAL INFORMATION:  
; APPLICANT: Bram, Richard J.  
; von Bulow, Gotz  
; TITLE OF INVENTION: A LYMPHOCYTE SURFACE RECEPTOR THAT BINDS  
; CAML, NUCLEIC ACIDS ENCODING THE SAME AND METHODS OF USE  
; THEREOF

NUMBER OF SEQUENCES: 11  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: David A. Jackson, Esq.  
STREET: 411 Hackensack Ave, Continental Plaza, 4th  
Floor

CITY: Hackensack  
STATE: New Jersey  
COUNTRY: USA  
ZIP: 07601

COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patent in Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/290,333  
FILING DATE: 12-Apr-1999  
CLASSIFICATION: <Unknown>  
ATTORNEY/AGENT INFORMATION:

NAME: Jackson Esq., David A.  
REGISTRATION NUMBER: 26,742  
REFERENCE/DOCKET NUMBER: 1340-1-007 PCT  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 201-487-5800  
TELEFAX: 201-343-1684

INFORMATION FOR SEQ ID NO: 6:  
SEQUENCE CHARACTERISTICS:

LENGTH: 166 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: peptide  
HYPOTHETICAL: NO  
FRAGMENT TYPE: N-terminal  
ORIGINAL SOURCE:

ORGANISM: Homo sapiens  
SEQUENCE DESCRIPTION: SEQ ID NO: 6:

US-09-290-333-6

Query Match 100.0%; Score 48; DB 3; Length 166;  
Best Local Similarity 100.0%; Pred. No. 0.7;  
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 SPVNLPEL 9  
Db 110 SPVNLPEL 118

## RESULT 3

US-09-782-857A-6  
; Sequence 6, Application US/09782857A  
; Patent No. 6500428  
; GENERAL INFORMATION:  
; APPLICANT: Bram, Richard J.  
; von Bulow, Gotz

TITLE OF INVENTION: A LYMPHOCYTE SURFACE RECEPTOR THAT BINDS

CAML, NUCLEIC ACIDS ENCODING THE SAME AND METHODS OF USE  
THEREOF

NUMBER OF SEQUENCES: 10  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: David A. Jackson, Esq.  
STREET: 411 Hackensack Ave, Continental Plaza, 4th  
Floor

CITY: Hackensack  
STATE: New Jersey  
COUNTRY: USA  
ZIP: 07601

COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patent in Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/782,857A  
FILING DATE: 14-Feb-2001  
CLASSIFICATION: <Unknown>

PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 08/810,572  
FILING DATE: <Unknown>

ATTORNEY/AGENT INFORMATION:  
NAME: Jackson Esq., David A.  
REGISTRATION NUMBER: 26,742  
REFERENCE/DOCKET NUMBER: 1340-1-007

TELECOMMUNICATION INFORMATION:  
TELEPHONE: 201-487-5800  
TELEFAX: 201-343-1684

INFORMATION FOR SEQ ID NO: 6:  
SEQUENCE CHARACTERISTICS:

LENGTH: 166 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: peptide  
HYPOTHETICAL: NO  
FRAGMENT TYPE: N-terminal  
ORIGINAL SOURCE:

ORGANISM: Homo sapiens  
SEQUENCE DESCRIPTION: SEQ ID NO: 6:

US-09-782-857A-6

Query Match 100.0%; Score 48; DB 4; Length 166;  
Best Local Similarity 100.0%; Pred. No. 0.7;  
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 SPVNLPEL 9  
Db 110 SPVNLPEL 118

## RESULT 4

US-09-854-864-15  
; Sequence 15, Application US/09854864  
; Patent No. 6774106  
; GENERAL INFORMATION:

APPLICANT: THEILL, LARS EYDE  
APPLICANT: YU, GANG

TITLE OF INVENTION: METHODS AND COMPOSITIONS OF MATTER CONCERNING APRIL/G70, BCMA,  
FILE REFERENCE: A-686B

CURRENT APPLICATION NUMBER: US/09/854,864  
CURRENT FILING DATE: 2001-09-11

PRIOR APPLICATION NUMBER: US 60/204,039  
PRIOR FILING DATE: 2000-05-12

PRIOR APPLICATION NUMBER: US 60/214,591  
PRIOR FILING DATE: 2000-06-27

NUMBER OF SEQ ID NOS: 31

SOFTWARE: Patent in version 3.1

SEQ ID NO 15

LENGTH: 166

; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-09-854-864-15

Query Match 100.0%; Score 48; DB 4; Length 166;  
Best Local Similarity 100.0%; Pred. No. 0.7; Indels 0; Gaps 0;  
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SPVNLPPPEL 9  
Db 110 SPVNLPPPEL 118

RESULT 5  
US-08-810-572A-2  
; Sequence 2, Application US/08810572A  
; Patent No. 5969102  
; GENERAL INFORMATION:  
; APPLICANT: Bram, Richard J.  
; APPLICANT: von Bulow, Gotz  
; TITLE OF INVENTION: A LYMPHOCYTE SURFACE RECEPTOR THAT BINDS  
; TITLE OF INVENTION: CAML, NUCLEIC ACIDS ENCODING THE SAME AND METHODS OF USE  
; NUMBER OF SEQUENCES: 11  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: David A. Jackson, Esq.  
; STREET: 411 Hackensack Ave, Continental Plaza, 4th  
; CITY: Hackensack  
; STATE: New Jersey  
; COUNTRY: USA  
; ZIP: 07601  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patent In Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/810,572A  
; FILING DATE: 28-FEB-1997  
; CLASSIFICATION: 536  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Jackson Esq., David A.  
; REGISTRATION NUMBER: 26,742  
; REFERENCE/DOCKET NUMBER: 1340-1-007  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 201-487-5800  
; TELEFAX: 201-343-1684  
; INFORMATION FOR SEQ ID NO: 2:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 293 amino acids  
; TYPE: amino acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: protein  
; HYPOTHETICAL: NO  
; FRAGMENT TYPE: N-terminal  
; ORIGINAL SOURCE:  
; ORGANISM: Homo sapiens  
US-08-810-572A-2

Query Match 100.0%; Score 48; DB 2; Length 293;  
Best Local Similarity 100.0%; Pred. No. 1.3; Indels 0; Gaps 0;  
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SPVNLPPPEL 9  
Db 110 SPVNLPPPEL 118

RESULT 6  
US-09-290-333-2  
; Sequence 2, Application US/09290333

; Patent No. 6316222  
; GENERAL INFORMATION:  
; APPLICANT: Bram, Richard J.  
; APPLICANT: von Bulow, Gotz  
; TITLE OF INVENTION: A LYMPHOCYTE SURFACE RECEPTOR THAT BINDS  
; TITLE OF INVENTION: CAML, NUCLEIC ACIDS ENCODING THE SAME AND METHODS OF USE  
; NUMBER OF SEQUENCES: 11  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: David A. Jackson, Esq.  
; STREET: 411 Hackensack Ave, Continental Plaza, 4th  
; CITY: Hackensack  
; STATE: New Jersey  
; COUNTRY: USA  
; ZIP: 07601  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patent In Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/09/290,333  
; FILING DATE: 12-Apr-1999  
; CLASSIFICATION: <Unknown>  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Jackson Esq., David A.  
; REGISTRATION NUMBER: 26,742  
; REFERENCE/DOCKET NUMBER: 1340-1-007 PCT  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 201-487-5800  
; TELEFAX: 201-343-1684  
; INFORMATION FOR SEQ ID NO: 2:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 293 amino acids  
; TYPE: amino acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: protein  
; HYPOTHETICAL: NO  
; FRAGMENT TYPE: N-terminal  
; ORIGINAL SOURCE:  
; ORGANISM: Homo sapiens  
; SEQUENCE DESCRIPTION: SEQ ID NO: 2:  
US-09-290-333-2

Query Match 100.0%; Score 48; DB 3; Length 293;  
Best Local Similarity 100.0%; Pred. No. 1.3; Indels 0; Gaps 0;  
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SPVNLPPPEL 9  
Db 110 SPVNLPPPEL 118

RESULT 7  
US-09-782-857A-2  
; Sequence 2, Application US/09782857A  
; Patent No. 6500428  
; GENERAL INFORMATION:  
; APPLICANT: Bram, Richard J.  
; APPLICANT: von Bulow, Gotz  
; TITLE OF INVENTION: A LYMPHOCYTE SURFACE RECEPTOR THAT BINDS  
; TITLE OF INVENTION: CAML, NUCLEIC ACIDS ENCODING THE SAME AND METHODS OF USE  
; NUMBER OF SEQUENCES: 10  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: David A. Jackson, Esq.  
; STREET: 411 Hackensack Ave, Continental Plaza, 4th  
; CITY: Hackensack  
; STATE: New Jersey  
; COUNTRY: USA

```
;
;
; ZIP: 07601
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/782,857A
; FILING DATE: 14-Feb-2001
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/810,572
; FILING DATE: <Unknown>
; ATTORNEY/AGENT INFORMATION:
; NAME: Jackson Esq., David A.
; REGISTRATION NUMBER: 26,742
; REFERENCE/DOCKET NUMBER: 1340-1-007
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 201-487-5800
; TELEFAX: 201-343-1684
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 293 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; HYPOTHEetical: NO
; FRAGMENT TYPE: N-terminal
; ORIGINAL SOURCE:
; ORGANISM: Homo sapiens
; SEQUENCE DESCRIPTION: SEQ ID NO: 2:
US-09-782-857A-2

Query Match 100.0%; Score 48; DB 4; Length 293;
Best Local Similarity 100.0%; Pred. No. 1.3;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 SPVNLPPPEL 9
Db 110 SPVNLPPPEL 118

RESULT 8
US-09-879-919-22
; Sequence 22, Application US/09879919
; Patent No. 6541224
; GENERAL INFORMATION:
; APPLICANT: Yu, Guo-Liang, et al.
; TITLE OF INVENTION: Human Tumor Necrosis Factor Delta and Epsilon
; FILE REFERENCE: PF253P1
; CURRENT APPLICATION NUMBER: US/09/879,919
; CURRENT FILING DATE: 2001-06-14
; PRIOR APPLICATION NUMBER: 60/293,499
; PRIOR FILING DATE: 2001-05-25
; PRIOR APPLICATION NUMBER: 60/277,978
; PRIOR FILING DATE: 2001-03-23
; PRIOR APPLICATION NUMBER: 60/276,248
; PRIOR FILING DATE: 2001-03-16
; PRIOR APPLICATION NUMBER: 60/254,875
; PRIOR FILING DATE: 2000-12-13
; PRIOR APPLICATION NUMBER: 60/241,952
; PRIOR FILING DATE: 2000-10-23
; PRIOR APPLICATION NUMBER: 60/211,537
; PRIOR FILING DATE: 2000-06-15
; PRIOR APPLICATION NUMBER: 08/815,783
; PRIOR FILING DATE: 1997-03-12
; PRIOR APPLICATION NUMBER: 60/016,812
; PRIOR FILING DATE: 1996-03-14
; NUMBER OF SEQ ID NOS: 26
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 22
; LENGTH: 293

Query Match 100.0%; Score 48; DB 4; Length 293;
Best Local Similarity 100.0%; Pred. No. 1.3;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 SPVNLPPPEL 9
Db 110 SPVNLPPPEL 118

RESULT 9
US-09-848-295-4
; Sequence 4, Application US/09848295
; Patent No. 6623941
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin
; APPLICANT: Ruben, Steven M.
; TITLE OF INVENTION: Human Tumor Necrosis Factor TR20 and Methods Based
; FILE REFERENCE: PF527
; CURRENT APPLICATION NUMBER: US/09/848,295
; CURRENT FILING DATE: 2001-05-04
; PRIOR APPLICATION NUMBER: 60/202,193
; PRIOR FILING DATE: 2000-05-05
; NUMBER OF SEQ ID NOS: 4
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 4
; LENGTH: 293
; TYPE: PRT
; ORGANISM: Homo sapiens
; SEQUENCE DESCRIPTION: SEQ ID NO: 4:
US-09-848-295-4

Query Match 100.0%; Score 48; DB 4; Length 293;
Best Local Similarity 100.0%; Pred. No. 1.3;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 SPVNLPPPEL 9
Db 110 SPVNLPPPEL 118

RESULT 10
US-09-854-864-14
; Sequence 14, Application US/09854864
; Patent No. 6774106
; GENERAL INFORMATION:
; APPLICANT: THEILL, LARS EYDE
; APPLICANT: YU, GANG
; TITLE OF INVENTION: METHODS AND COMPOSITIONS OF MATTER CONCERNING APRIL/G70, BCMA,
; FILE REFERENCE: BLYS/AGP-3, AND TACI
; FILE REFERENCE: A-686B
; CURRENT APPLICATION NUMBER: US/09/854,864
; CURRENT FILING DATE: 2001-09-11
; PRIOR APPLICATION NUMBER: US 60/204,039
; PRIOR FILING DATE: 2000-05-12
; PRIOR APPLICATION NUMBER: US 60/214,591
; PRIOR FILING DATE: 2000-06-27
; NUMBER OF SEQ ID NOS: 31
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 14
; LENGTH: 293
; TYPE: PRT
; ORGANISM: Homo sapiens
; SEQUENCE DESCRIPTION: SEQ ID NO: 14:
US-09-854-864-14

Query Match 100.0%; Score 48; DB 4; Length 293;
Best Local Similarity 100.0%; Pred. No. 1.3;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 SPVNLPPPEL 9
```

```
Db      110 SPVNLPEL 118
|||||
US-09-854-864-18
; Sequence 18, Application US/09854864
; Patent No. 6774106
; GENERAL INFORMATION:
; APPLICANT: THEILL, LARS EYDE
; APPLICANT: YU, GANG
; TITLE OF INVENTION: METHODS AND COMPOSITIONS OF MATTER CONCERNING APRIL/G70, BCWA,
; TITLE OF INVENTION: BLYS/AGP-3, AND TACI
; FILE REFERENCE: A-686B
; CURRENT APPLICATION NUMBER: US/09/854,864
; PRIOR FILING DATE: 2001-09-11
; PRIOR APPLICATION NUMBER: US 60/204,039
; PRIOR FILING DATE: 2000-05-12
; PRIOR APPLICATION NUMBER: US 60/214,591
; PRIOR FILING DATE: 2000-06-27
; NUMBER OF SEQ ID NOS: 31
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 18
; LENGTH: 397
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-854-864-18

Query Match      100.0%; Score 48; DB 4; Length 397;
Best Local Similarity 100.0%; Pred. No. 1.8;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 SPVNLPEL 9
|||||
Db      110 SPVNLPEL 118

RESULT 12
US-09-248-796A-19216
; Sequence 19216, Application US/09248796A
; Patent No. 6747137
; GENERAL INFORMATION:
; APPLICANT: Keith Weinstock et al
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO CANDIDA ALBICAN
; TITLE OF INVENTION: FOR DIAGNOSTICS AND THERAPEUTICS
; FILE REFERENCE: 107196.132
; CURRENT APPLICATION NUMBER: US/09/248,796A
; CURRENT FILING DATE: 1999-02-12
; PRIOR APPLICATION NUMBER: US 60/074,725
; PRIOR FILING DATE: 1998-02-13
; PRIOR APPLICATION NUMBER: US 60/096,409
; PRIOR FILING DATE: 1998-08-13
; NUMBER OF SEQ ID NOS: 28208
; SEQ ID NO 19216
; LENGTH: 456
; TYPE: PRT
; ORGANISM: Candida albicans
; FEATURE:
; NAME/KEY: UNSURE
; LOCATION: (389)
; OTHER INFORMATION: Identity of amino acid sequences at the above locations are unkno
US-09-248-796A-19216

Query Match      83.3%; Score 40; DB 4; Length 456;
Best Local Similarity 100.0%; Pred. No. 44;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      2 PVNLPPE 8
|||||
Db      255 PVNLPPE 261

RESULT 13
US-09-485-621-2
; Sequence 2, Application US/08485621
; Patent No. 5691187
; GENERAL INFORMATION:
; APPLICANT: Kmiec, Eric B.
; APPLICANT: Gerhold, David L.
; APPLICANT: Strauss, Allyson Cole
; TITLE OF INVENTION: Anti-fungal Agents and Methods of
; TITLE OF INVENTION: Identifying and Using the Same
; NUMBER OF SEQUENCES: 2
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Woodcock Washburn Kurtz Mackiewicz &
; ADDRESSEE: No. 5942386ris
; STREET: One Liberty Place, 46th floor
; CITY: Philadelphia
; STATE: Pennsylvania
; COUNTRY: U.S.A.
; ZIP: 19103
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/485,621
; FILING DATE:
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Deluca, Mark
; REGISTRATION NUMBER: 33,229
; REFERENCE/DOCKET NUMBER: TJU-1584
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 215-568-3100
; TELEFAX: 215-568-3439
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 780 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-485-621-2

Query Match      83.3%; Score 40; DB 1; Length 780;
Best Local Similarity 100.0%; Pred. No. 77;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      2 PVNLPPE 8
|||||
Db      188 PVNLPPE 194

RESULT 14
US-08-973-831-2
; Sequence 2, Application US/08973831
; Patent No. 5942386
; GENERAL INFORMATION:
; APPLICANT: Kmiec, Eric B.
; APPLICANT: Gerhold, David L.
; APPLICANT: Strauss, Allyson Cole
; TITLE OF INVENTION: Anti-fungal Agents and Methods of
; TITLE OF INVENTION: Identifying and Using the Same
; NUMBER OF SEQUENCES: 2
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Woodcock Washburn Kurtz Mackiewicz &
; ADDRESSEE: No. 5942386ris
; STREET: One Liberty Place, 46th floor
; CITY: Philadelphia
; STATE: Pennsylvania
; COUNTRY: U.S.A.
; ZIP: 19103
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
```

OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/973,831  
FILING DATE:  
CLASSIFICATION:  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 08/485,621  
FILING DATE:  
ATTORNEY/AGENT INFORMATION:  
NAME: Deluca, Mark  
REGISTRATION NUMBER: 33,229  
REFERENCE/DOCKET NUMBER: TJU-1584  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 215-568-3100  
TELEFAX: 215-568-3439  
INFORMATION FOR SEQ ID NO: 2:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 780 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
US-08-973-831-2

Query Match 83.3%; Score 40; DB 2; Length 780;  
Best Local Similarity 100.0%; Pred. No. 77;  
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 PVLNLPPE 8  
Db 188 PVLNLPPE 194

## RESULT 15

PCT-US96-09530A-2  
Sequence 2, Application PC/TUS9609530A  
GENERAL INFORMATION:  
APPLICANT: Kmiec, Eric B.  
APPLICANT: Gerhold, David L.  
APPLICANT: Strauss, Allyson Cole  
TITLE OF INVENTION: Anti-fungal Agents and Methods of  
TITLE OF INVENTION: Identifying and Using the Same  
NUMBER OF SEQUENCES: 2  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Woodcock Washburn Kurtz Mackiewicz & Norris  
STREET: One Liberty Place, 46th floor  
CITY: Philadelphia  
STATE: Pennsylvania  
COUNTRY: U.S.A.  
ZIP: 19103  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Wordperfect 6.1  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: PCT/US96/09530A  
FILING DATE:  
CLASSIFICATION:  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/485,621  
FILING DATE: 07-JUN-1995  
CLASSIFICATION:  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 60/000,399  
FILING DATE: 21-JUN-1995  
CLASSIFICATION:  
ATTORNEY/AGENT INFORMATION:  
NAME: Deluca, Mark  
REGISTRATION NUMBER: 33,229  
REFERENCE/DOCKET NUMBER: TJU-1970  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 215-568-3100

TELEFAX: 215-568-3439  
INFORMATION FOR SEQ ID NO: 2:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 780 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
PCT-US96-09530A-2

Query Match 83.3%; Score 40; DB 5; Length 780;  
Best Local Similarity 100.0%; Pred. No. 77;  
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 PVLNLPPE 8  
Db 188 PVLNLPPE 194

Search completed: November 19, 2004, 23:45:58  
Job time : 11.0986 secs

GenCore version 5.1.6  
Copyright (c) 1993 - 2004 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: November 19, 2004, 23:40:10 ; Search time 24.4648 Seconds  
(without alignments)  
130.275 Million cell updates/sec

Title: US-10-068-725-4\_COPY\_110\_118

Perfect score: 48  
Sequence: 1 SPVNLPPPEL 9

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 1570615 seqs, 354127592 residues

Total number of hits satisfying chosen parameters: 1570615

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : Published Applications AA.\*  
1: /cgn2\_6/ptodata/2/pubpaa/US07\_PUBCOMB.pep.\*  
2: /cgn2\_6/ptodata/2/pubpaa/US07\_PUBCOMB.pep.\*  
3: /cgn2\_6/ptodata/2/pubpaa/US06\_NEW\_PUB.pep.\*  
4: /cgn2\_6/ptodata/2/pubpaa/US06\_NEW\_PUB.pep.\*  
5: /cgn2\_6/ptodata/2/pubpaa/US07\_NEW\_PUB.pep.\*  
6: /cgn2\_6/ptodata/2/pubpaa/US07\_NEW\_PUB.pep.\*  
7: /cgn2\_6/ptodata/2/pubpaa/US08\_NEW\_PUB.pep.\*  
8: /cgn2\_6/ptodata/2/pubpaa/US08\_NEW\_PUB.pep.\*  
9: /cgn2\_6/ptodata/2/pubpaa/US09A\_PUBCOMB.pep.\*  
10: /cgn2\_6/ptodata/2/pubpaa/US09B\_PUBCOMB.pep.\*  
11: /cgn2\_6/ptodata/2/pubpaa/US09C\_PUBCOMB.pep.\*  
12: /cgn2\_6/ptodata/2/pubpaa/US09\_NEW\_PUB.pep.\*  
13: /cgn2\_6/ptodata/2/pubpaa/US10A\_PUBCOMB.pep.\*  
14: /cgn2\_6/ptodata/2/pubpaa/US10B\_PUBCOMB.pep.\*  
15: /cgn2\_6/ptodata/2/pubpaa/US10C\_PUBCOMB.pep.\*  
16: /cgn2\_6/ptodata/2/pubpaa/US10D\_PUBCOMB.pep.\*  
17: /cgn2\_6/ptodata/2/pubpaa/US10\_NEW\_PUB.pep.\*  
18: /cgn2\_6/ptodata/2/pubpaa/US11\_NEW\_PUB.pep.\*  
19: /cgn2\_6/ptodata/2/pubpaa/US60\_NEW\_PUB.pep.\*  
20: /cgn2\_6/ptodata/2/pubpaa/US60\_PUBCOMB.pep.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

| Result No. | Score | Query Match | Length | ID                    | Description       |
|------------|-------|-------------|--------|-----------------------|-------------------|
| 1          | 48    | 100.0       | 57     | 9 US-09-779-050A-47   | Sequence 47, Appl |
| 2          | 48    | 100.0       | 166    | 9 US-09-854-864-15    | Sequence 15, Appl |
| 3          | 48    | 100.0       | 166    | 9 US-09-855-158-15    | Sequence 15, Appl |
| 4          | 48    | 100.0       | 166    | 14 US-10-293-816-6    | Sequence 6, Appli |
| 5          | 48    | 100.0       | 291    | 9 US-09-779-050A-43   | Sequence 43, Appl |
| 6          | 48    | 100.0       | 293    | 9 US-09-879-919-22    | Sequence 22, Appl |
| 7          | 48    | 100.0       | 293    | 9 US-09-854-864-14    | Sequence 14, Appl |
| 8          | 48    | 100.0       | 293    | 9 US-09-855-158-14    | Sequence 14, Appl |
| 9          | 48    | 100.0       | 293    | 9 US-09-961-376-2     | Sequence 2, Appli |
| 10         | 48    | 100.0       | 293    | 9 US-09-779-050A-42   | Sequence 42, Appl |
| 11         | 48    | 100.0       | 293    | 10 US-09-302-863-2    | Sequence 2, Appli |
| 12         | 48    | 100.0       | 293    | 10 US-09-855-564-2    | Sequence 2, Appli |
| 13         | 48    | 100.0       | 293    | 13 US-10-087-192-1650 | Sequence 1650, Ap |

|    |    |       |      |    |                      |                   |
|----|----|-------|------|----|----------------------|-------------------|
| 14 | 48 | 100.0 | 293  | 13 | US-10-084-971-2      | Sequence 2, Appli |
| 15 | 48 | 100.0 | 293  | 14 | US-10-068-725-4      | Sequence 4, Appli |
| 16 | 48 | 100.0 | 293  | 14 | US-10-151-882-46     | Sequence 46, Appl |
| 17 | 48 | 100.0 | 293  | 14 | US-10-293-816-2      | Sequence 2, Appli |
| 18 | 48 | 100.0 | 293  | 14 | US-10-008-063-8      | Sequence 8, Appli |
| 19 | 48 | 100.0 | 293  | 14 | US-10-152-363A-2     | Sequence 2, Appli |
| 20 | 48 | 100.0 | 293  | 14 | US-10-268-951-22     | Sequence 22, Appl |
| 21 | 48 | 100.0 | 293  | 15 | US-10-258-368-1      | Sequence 1, Appli |
| 22 | 48 | 100.0 | 293  | 15 | US-10-618-797-4      | Sequence 4, Appli |
| 23 | 48 | 100.0 | 293  | 17 | US-10-743-634-7      | Sequence 7, Appli |
| 24 | 48 | 100.0 | 293  | 17 | US-10-748-112-27     | Sequence 27, Appl |
| 25 | 48 | 100.0 | 301  | 15 | US-10-258-368-12     | Sequence 12, Appl |
| 26 | 48 | 100.0 | 357  | 14 | US-10-152-363A-56    | Sequence 56, Appl |
| 27 | 48 | 100.0 | 392  | 14 | US-10-152-363A-50    | Sequence 50, Appl |
| 28 | 48 | 100.0 | 397  | 9  | US-09-854-864-18     | Sequence 18, Appl |
| 29 | 48 | 100.0 | 397  | 9  | US-09-855-158-18     | Sequence 18, Appl |
| 30 | 48 | 100.0 | 404  | 15 | US-10-258-368-15     | Sequence 15, Appl |
| 31 | 43 | 89.6  | 538  | 17 | US-10-425-115-271495 | Sequence 271495,  |
| 32 | 40 | 83.3  | 519  | 17 | US-10-425-115-221726 | Sequence 221726,  |
| 33 | 39 | 81.2  | 452  | 15 | US-10-424-599-216836 | Sequence 216836,  |
| 34 | 39 | 81.2  | 905  | 16 | US-10-451-457A-64    | Sequence 64, Appl |
| 35 | 39 | 81.2  | 1081 | 17 | US-10-425-115-217364 | Sequence 217364,  |
| 36 | 39 | 81.2  | 1304 | 17 | US-10-425-115-217365 | Sequence 217365,  |
| 37 | 39 | 81.2  | 1438 | 17 | US-10-425-115-217361 | Sequence 217361,  |
| 38 | 39 | 81.2  | 1540 | 17 | US-10-425-115-217355 | Sequence 217355,  |
| 39 | 39 | 81.2  | 1606 | 17 | US-10-425-115-217360 | Sequence 217360,  |
| 40 | 39 | 81.2  | 1742 | 17 | US-10-425-115-254920 | Sequence 254920,  |
| 41 | 39 | 81.2  | 1753 | 17 | US-10-425-115-254923 | Sequence 254923,  |
| 42 | 38 | 79.2  | 157  | 17 | US-10-425-115-246652 | Sequence 246652,  |
| 43 | 38 | 79.2  | 267  | 16 | US-10-437-963-194387 | Sequence 194387,  |
| 44 | 38 | 79.2  | 333  | 14 | US-10-369-493-20124  | Sequence 20124, A |
| 45 | 38 | 79.2  | 346  | 14 | US-10-369-493-18841  | Sequence 18841, A |

#### ALIGNMENTS

RESULT 1  
US-09-779-050A-47  
; Sequence 47, Application US/09779050A  
; Patent No. US20020160416A1  
; GENERAL INFORMATION:  
; APPLICANT: BOYLE, WILLIAM  
; APPLICANT: HSU, HAILING  
; TITLE OF INVENTION: RECEPTOR FROM TNF FAMILY  
; FILE REFERENCE: A-570B  
; CURRENT APPLICATION NUMBER: US/09/779,050A  
; CURRENT FILING DATE: 2001-02-12  
; PRIOR APPLICATION NUMBER: 60/181,800  
; PRIOR FILING DATE: 2000-02-11  
; NUMBER OF SEQ ID NOS: 52  
; SOFTWARE: PatentIn version 3.0  
; SEQ ID NO 47  
; LENGTH: 57  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-09-779-050A-47

Query Match 100.0%; Score 48; DB 9; Length 57;  
Best Local Similarity 100.0%; Pred. No. 3.5;  
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
  
QY 1 SPVNLPPPEL 9  
Db 3 SPVNLPPPEL 11  
  
RESULT 2  
US-09-854-864-15  
; Sequence 15, Application US/09854864  
; Patent No. US20020081296A1  
; GENERAL INFORMATION:  
; APPLICANT: THEILL, LARS EYDE

```
; APPLICANT: YU, GANG
; TITLE OF INVENTION: METHODS AND COMPOSITIONS OF MATTER CONCERNING APRIL/G70, BCMA,
; FILE REFERENCE: A-686B
; CURRENT APPLICATION NUMBER: US/09/854,864
; CURRENT FILING DATE: 2001-09-11
; PRIOR APPLICATION NUMBER: US 60/204,039
; PRIOR FILING DATE: 2000-05-12
; PRIOR APPLICATION NUMBER: US 60/214,591
; PRIOR FILING DATE: 2000-06-27
; NUMBER OF SEQ ID NOS: 31
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 15
; LENGTH: 166
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-854-864-15

Query Match      100.0%; Score 48; DB 9; Length 166;
Best Local Similarity 100.0%; Pred. No. 10;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 SPVNLPPPEL 9
Db      110 SPVNLPPPEL 118

RESULT 3
US-09-855-158-15
; Sequence 15, Application US/09855158
; Publication No. US20020086018A1
; GENERAL INFORMATION:
; APPLICANT: THEILL, LARS EYDE
; APPLICANT: YU, GANG
; TITLE OF INVENTION: METHODS AND COMPOSITIONS OF MATTER CONCERNING APRIL/G70, BCMA, BL
; FILE REFERENCE: A-686A
; CURRENT APPLICATION NUMBER: US/09/855,158
; CURRENT FILING DATE: 2001-09-11
; PRIOR APPLICATION NUMBER: US 60/214,591
; PRIOR FILING DATE: 2000-06-27
; PRIOR APPLICATION NUMBER: US 60/204,039
; PRIOR FILING DATE: 2000-05-12
; NUMBER OF SEQ ID NOS: 30
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 15
; LENGTH: 166
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-855-158-15

Query Match      100.0%; Score 48; DB 9; Length 166;
Best Local Similarity 100.0%; Pred. No. 10;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 SPVNLPPPEL 9
Db      110 SPVNLPPPEL 118

RESULT 4
US-10-293-816-6
; Sequence 6, Application US/10293816
; Publication No. US20030082173A1
; GENERAL INFORMATION:
; APPLICANT: Bram, Richard J.
; APPLICANT: Von Bulow, Gotz
; TITLE OF INVENTION: A LYMPHOCYTE SURFACE RECEPTOR THAT BINDS
; TITLE OF INVENTION: CAML AND METHODS OF USE THEREOF
; FILE REFERENCE: 44158/254623
; CURRENT APPLICATION NUMBER: US/10/293,816
; CURRENT FILING DATE: 2002-11-12
; PRIOR APPLICATION NUMBER: US 09/782,857
```

```
; PRIOR FILING DATE: 2001-02-14
; PRIOR APPLICATION NUMBER: US 09/290,333
; PRIOR FILING DATE: 1999-04-12
; PRIOR APPLICATION NUMBER: US 08/810,572
; PRIOR FILING DATE: 1997-03-03
; NUMBER OF SEQ ID NOS: 11
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 6
; LENGTH: 166
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-293-816-6

Query Match      100.0%; Score 48; DB 14; Length 166;
Best Local Similarity 100.0%; Pred. No. 10;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 SPVNLPPPEL 9
Db      110 SPVNLPPPEL 118

RESULT 5
US-09-779-050A-43
; Sequence 43, Application US/09779050A
; Patent No. US20020160416A1
; GENERAL INFORMATION:
; APPLICANT: BOYLE, WILLIAM
; APPLICANT: HSU, HAILING
; TITLE OF INVENTION: RECEPTOR FROM TNF FAMILY
; FILE REFERENCE: A-570B
; CURRENT APPLICATION NUMBER: US/09/779,050A
; CURRENT FILING DATE: 2001-02-12
; PRIOR APPLICATION NUMBER: 60/181,800
; PRIOR FILING DATE: 2000-02-11
; NUMBER OF SEQ ID NOS: 52
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 43
; LENGTH: 291
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-779-050A-43

Query Match      100.0%; Score 48; DB 9; Length 291;
Best Local Similarity 100.0%; Pred. No. 17;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 SPVNLPPPEL 9
Db      110 SPVNLPPPEL 118

RESULT 6
US-09-879-919-22
; Sequence 22, Application US/09879919
; Patent No. US20020064829A1
; GENERAL INFORMATION:
; APPLICANT: Yu, Guo-Liang, et al.
; TITLE OF INVENTION: Human Tumor Necrosis Factor Delta and Epsilon
; FILE REFERENCE: PF253P1
; CURRENT APPLICATION NUMBER: US/09/879,919
; CURRENT FILING DATE: 2001-06-14
; PRIOR APPLICATION NUMBER: 60/293,499
; PRIOR FILING DATE: 2001-05-25
; PRIOR APPLICATION NUMBER: 60/277,978
; PRIOR FILING DATE: 2001-03-23
; PRIOR APPLICATION NUMBER: 60/276,248
; PRIOR FILING DATE: 2001-03-16
; PRIOR APPLICATION NUMBER: 60/254,875
; PRIOR FILING DATE: 2000-12-13
; PRIOR APPLICATION NUMBER: 60/241,952
; PRIOR FILING DATE: 2000-10-23
; PRIOR APPLICATION NUMBER: 60/211,537
```



; PRIOR FILING DATE: 2000-06-15  
; PRIOR APPLICATION NUMBER: 08/815,783  
; PRIOR FILING DATE: 1997-03-12  
; PRIOR APPLICATION NUMBER: 60/016,812  
; PRIOR FILING DATE: 1996-03-14  
; NUMBER OF SEQ ID NOS: 26  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 22  
; LENGTH: 293  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-09-879-919-22

Query Match 100.0%; Score 48; DB 9; Length 293;  
Best Local Similarity 100.0%; Pred. No. 17;  
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SPVNLPPPEL 9  
Db 110 SPVNLPPPEL 118

## RESULT 7

; Sequence 14, Application US/09854864  
; Patent No. US20020081296A1  
; GENERAL INFORMATION:  
; APPLICANT: THEILL, LARS EYDE  
; APPLICANT: YU, GANG  
; TITLE OF INVENTION: METHODS AND COMPOSITIONS OF MATTER CONCERNING APRIL/G70, BCMA,  
; FILE REFERENCE: BUYS/AGP-3, AND TACI  
; CURRENT APPLICATION NUMBER: US/09/854,864  
; PRIOR FILING DATE: 2001-09-11  
; PRIOR APPLICATION NUMBER: US 60/204,039  
; PRIOR FILING DATE: 2000-05-12  
; PRIOR APPLICATION NUMBER: US 60/214,591  
; PRIOR FILING DATE: 2000-06-27  
; NUMBER OF SEQ ID NOS: 31  
; SOFTWARE: PatentIn version 3.1  
; SEQ ID NO 14  
; LENGTH: 293  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-09-854-864-14

Query Match 100.0%; Score 48; DB 9; Length 293;  
Best Local Similarity 100.0%; Pred. No. 17;  
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SPVNLPPPEL 9  
Db 110 SPVNLPPPEL 118

## RESULT 8

; Sequence 14, Application US/09855158  
; Publication No. US20020086018A1  
; GENERAL INFORMATION:  
; APPLICANT: THEILL, LARS EYDE  
; APPLICANT: YU, GANG  
; TITLE OF INVENTION: METHODS AND COMPOSITIONS OF MATTER CONCERNING APRIL/G70, BCMA, BL  
; FILE REFERENCE: A-686A  
; CURRENT APPLICATION NUMBER: US/09/855,158  
; CURRENT FILING DATE: 2001-09-11  
; PRIOR APPLICATION NUMBER: US 60/214,591  
; PRIOR FILING DATE: 2000-06-27  
; PRIOR APPLICATION NUMBER: US 60/204,039  
; PRIOR FILING DATE: 2000-05-12  
; NUMBER OF SEQ ID NOS: 30  
; SOFTWARE: PatentIn version 3.1

; SEQ ID NO 14  
; LENGTH: 293  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-09-855-158-14

Query Match 100.0%; Score 48; DB 9; Length 293;  
Best Local Similarity 100.0%; Pred. No. 17;  
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SPVNLPPPEL 9  
Db 110 SPVNLPPPEL 118

## RESULT 9

; Sequence 2, Application US/09961376  
; Patent No. US20020106736A1  
; GENERAL INFORMATION:  
; APPLICANT: Ruben et al.  
; TITLE OF INVENTION: Human Tumor Necrosis Factor Receptor TR17  
; FILE REFERENCE: PF524P1  
; CURRENT APPLICATION NUMBER: US/09/961,376  
; CURRENT FILING DATE: 2001-09-25  
; PRIOR APPLICATION NUMBER: 60/254,874  
; PRIOR FILING DATE: 2000-12-13  
; PRIOR APPLICATION NUMBER: 60/235,991  
; PRIOR FILING DATE: 2000-09-26  
; PRIOR APPLICATION NUMBER: 09/533,822  
; PRIOR FILING DATE: 2000-03-24  
; PRIOR APPLICATION NUMBER: 60/188,208  
; PRIOR FILING DATE: 2000-03-10  
; NUMBER OF SEQ ID NOS: 7  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 2  
; LENGTH: 293  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-09-961-376-2

Query Match 100.0%; Score 48; DB 9; Length 293;  
Best Local Similarity 100.0%; Pred. No. 17;  
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SPVNLPPPEL 9  
Db 110 SPVNLPPPEL 118

## RESULT 10

; Sequence 42, Application US/09779050A  
; Patent No. US20020160416A1  
; GENERAL INFORMATION:  
; APPLICANT: BOYLE, WILLIAM  
; APPLICANT: HSU, HAILING  
; TITLE OF INVENTION: RECEPTOR FROM TNF FAMILY  
; FILE REFERENCE: A-570B  
; CURRENT APPLICATION NUMBER: US/09/779,050A  
; CURRENT FILING DATE: 2001-02-12  
; PRIOR APPLICATION NUMBER: 60/181,800  
; PRIOR FILING DATE: 2000-02-11  
; NUMBER OF SEQ ID NOS: 52  
; SOFTWARE: PatentIn version 3.0  
; SEQ ID NO 42  
; LENGTH: 293  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-09-779-050A-42

Query Match 100.0%; Score 48; DB 9; Length 293;  
Best Local Similarity 100.0%; Pred. No. 17;

Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 SPVNLPPPEL 9  
| | | | |  
Db 110 SPVNLPPPEL 118

## RESULT 11

US-09-302-863-2  
; Sequence 2, Application US/09302863  
; Publication No. US2003002233A1  
; GENERAL INFORMATION:  
; APPLICANT: Goodwin, Raymond G  
; APPLICANT: Din, Wanwan S.  
; TITLE OF INVENTION: METHODS OF USE OF THE TAC1/TAC1-L INTERACTION  
; FILE REFERENCE: 2519  
; CURRENT APPLICATION NUMBER: US/09/302,863  
; CURRENT FILING DATE: 1999-04-30  
; NUMBER OF SEQ ID NOS: 5  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 2  
; LENGTH: 293  
; TYPE: PRT  
; ORGANISM: Human  
US-09-302-863-2

Query Match 100.0%; Score 48; DB 10; Length 293;  
Best Local Similarity 100.0%; Pred. No. 17;  
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 SPVNLPPPEL 9  
| | | | |  
Db 110 SPVNLPPPEL 118

## RESULT 12

US-09-855-564-2  
; Sequence 2, Application US/09855564  
; Publication No. US20030165986A1  
; GENERAL INFORMATION:  
; APPLICANT: Goodwin, Raymond G  
; APPLICANT: Din, Wanwan S.  
; TITLE OF INVENTION: METHODS OF USE OF THE TAC1/TAC1-L INTERACTION  
; FILE REFERENCE: 2519  
; CURRENT APPLICATION NUMBER: US/09/855,564  
; CURRENT FILING DATE: 2001-05-14  
; PRIOR APPLICATION NUMBER: 09/302,863  
; PRIOR FILING DATE: 1999-04-30  
; NUMBER OF SEQ ID NOS: 5  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 2  
; LENGTH: 293  
; TYPE: PRT  
; ORGANISM: Human  
US-09-855-564-2

Query Match 100.0%; Score 48; DB 10; Length 293;  
Best Local Similarity 100.0%; Pred. No. 17;  
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 SPVNLPPPEL 9  
| | | | |  
Db 110 SPVNLPPPEL 118

## RESULT 13

US-10-087-192-1650  
; Sequence 1650, Application US/10087192  
; Publication No. US20020182586A1  
; GENERAL INFORMATION:  
; APPLICANT: Morris, David W.  
; APPLICANT: Engelhard, Eric K.  
; TITLE OF INVENTION: NOVEL COMPOSITIONS AND METHODS FOR

; TITLE OF INVENTION: CANCER  
; FILE REFERENCE: 529452000122  
; CURRENT APPLICATION NUMBER: US/10/087,192  
; CURRENT FILING DATE: 2002-03-01  
; PRIOR APPLICATION NUMBER: US 09/747,377  
; PRIOR FILING DATE: 2000-12-22  
; PRIOR APPLICATION NUMBER: US 09/798,586  
; PRIOR FILING DATE: 2001-03-02  
; NUMBER OF SEQ ID NOS: 2059  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 1650  
; LENGTH: 293  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-10-087-192-1650

Query Match 100.0%; Score 48; DB 13; Length 293;  
Best Local Similarity 100.0%; Pred. No. 17;  
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 SPVNLPPPEL 9  
| | | | |  
Db 110 SPVNLPPPEL 118

## RESULT 14

US-10-084-971-2  
; Sequence 2, Application US/10084971  
; Publication No. US20020187526A1  
; GENERAL INFORMATION:  
; APPLICANT: Human Genome Sciences, Inc.  
; TITLE OF INVENTION: Neutrokin-alpha Binding Proteins and Methods Based Thereon  
; FILE REFERENCE: PF524PCT  
; CURRENT APPLICATION NUMBER: US/10/084,971  
; CURRENT FILING DATE: 2002-03-01  
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: US/09/533,822  
; PRIOR FILING DATE: EARLIER FILING DATE: 2000-03-24  
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 60/126,599  
; PRIOR FILING DATE: EARLIER FILING DATE: 1999-03-26  
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 60/188,208  
; PRIOR FILING DATE: EARLIER FILING DATE: 1999-03-10  
; NUMBER OF SEQ ID NOS: 5  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 2  
; LENGTH: 293  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-10-084-971-2

Query Match 100.0%; Score 48; DB 13; Length 293;  
Best Local Similarity 100.0%; Pred. No. 17;  
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 SPVNLPPPEL 9  
| | | | |  
Db 110 SPVNLPPPEL 118

## RESULT 15

US-10-068-725-4  
; Sequence 4, Application US/10068725  
; Publication No. US20030012783A1  
; GENERAL INFORMATION:  
; APPLICANT: Kindsvogel, Wayne  
; TITLE OF INVENTION: Antibodies That Bind Both BCMA and TAC1  
; FILE REFERENCE: 01-04  
; CURRENT APPLICATION NUMBER: US/10/068,725  
; CURRENT FILING DATE: 2002-02-06  
; PRIOR APPLICATION NUMBER: 60/270,274  
; PRIOR FILING DATE: 2001-02-20  
; PRIOR APPLICATION NUMBER: 60/283,447  
; PRIOR FILING DATE: 2001-04-12  
; NUMBER OF SEQ ID NOS: 5

```
; SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 4
; LENGTH: 293
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-068-725-4
```

```
Query Match      100.0%; Score 48; DB 14; Length 293;
Best Local Similarity 100.0%; Pred. No. 17;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
QY      1 SPVNLPPPEL 9
      |||||
Db      110 SPVNLPPPEL 118
```

```
Search completed: November 20, 2004, 00:00:28
Job time : 24.4648 secs
```

**this Page Blank (uspto)**

GenCore version 5.1.6  
Copyright (c) 1993 - 2004 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: November 19, 2004, 23:34:49 ; Search time 3.29577 Seconds  
(without alignments)  
262.746 Million cell updates/sec

Title: US-10-068-725-4\_COPY\_110\_118  
Perfect score: 48  
Sequence: 1 SPVNLPPPEL 9

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0  
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : PIR 79:.\*  
1: pir1:.\*  
2: pir2:.\*  
3: pir3:.\*  
4: pir4:.\*

Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Score | Query Match | Length | ID       | Description        |
|------------|-------|-------------|--------|----------|--------------------|
| 1          | 41    | 85.4        | 812    | 1 ISZPT1 | DNA topoisomerase  |
| 2          | 41    | 85.4        | 814    | 2 T50327 | dna topoisomerase  |
| 3          | 40    | 83.3        | 1011   | 2 T17430 | tol protein - Neur |
| 4          | 39    | 81.2        | 905    | 1 RBYSS  | regulatory protein |
| 5          | 38    | 79.2        | 277    | 2 I38857 | microtubule-associ |
| 6          | 38    | 79.2        | 384    | 2 AF2426 | histidinol-phospha |
| 7          | 38    | 79.2        | 2774   | 2 A43359 | microtubule-associ |
| 8          | 37    | 77.1        | 323    | 2 A9624  | NADH dehydrogenase |
| 9          | 37    | 77.1        | 323    | 2 A9622  | NADH dehydrogenase |
| 10         | 37    | 77.1        | 324    | 2 A9616  | NADH dehydrogenase |
| 11         | 37    | 77.1        | 324    | 2 T11167 | NADH dehydrogenase |
| 12         | 37    | 77.1        | 328    | 2 G96519 | hypothetical prote |
| 13         | 37    | 77.1        | 360    | 2 G72235 | hypothetical prote |
| 14         | 37    | 77.1        | 604    | 2 S58643 | probable transcrip |
| 15         | 37    | 77.1        | 1082   | 2 H81982 | hypothetical prote |
| 16         | 36    | 75.0        | 53     | 2 A61219 | serpin Spi 1 - hor |
| 17         | 36    | 75.0        | 54     | 2 S14338 | serpin I - horse ( |
| 18         | 36    | 75.0        | 257    | 2 T40880 | hypothetical prote |
| 19         | 36    | 75.0        | 448    | 2 A70578 | probable dap2 pro  |
| 20         | 36    | 75.0        | 467    | 2 B87070 | probable peptidase |
| 21         | 36    | 75.0        | 514    | 2 A36793 | hypothetical prote |
| 22         | 36    | 75.0        | 563    | 2 T44214 | probable phosphor  |
| 23         | 36    | 75.0        | 563    | 2 T44029 | Ganciclovir kinase |
| 24         | 36    | 75.0        | 656    | 2 AF1040 | Vi polysaccharide  |
| 25         | 36    | 75.0        | 656    | 2 A56975 | Vi polysaccharide  |
| 26         | 36    | 75.0        | 947    | 2 I49635 | mouse Dhml protein |
| 27         | 36    | 75.0        | 962    | 2 S58107 | hypothetical WD-40 |
| 28         | 36    | 75.0        | 1188   | 2 S49915 | extensin-like prot |
| 29         | 36    | 75.0        | 1706   | 2 B75633 | probable RNA helic |

|    |    |      |      |          |                    |
|----|----|------|------|----------|--------------------|
| 30 | 36 | 75.0 | 1791 | 2 T02909 | hypothetical prote |
| 31 | 36 | 75.0 | 1939 | 2 AF0095 | probable sideroph  |
| 32 | 35 | 72.9 | 51   | 2 B61219 | serpin Spi 2 - hor |
| 33 | 35 | 72.9 | 172  | 2 T21753 | hypothetical prote |
| 34 | 35 | 72.9 | 295  | 2 C87599 | conserved hypothet |
| 35 | 35 | 72.9 | 345  | 2 G75202 | dipeptide abc tran |
| 36 | 35 | 72.9 | 477  | 2 G83048 | probable two-compo |
| 37 | 35 | 72.9 | 711  | 1 S28391 | protein-tyrosine-p |
| 38 | 35 | 72.9 | 711  | 2 T45160 | protein-tyrosine-p |
| 39 | 35 | 72.9 | 744  | 2 T20969 | hypothetical prote |
| 40 | 35 | 72.9 | 823  | 2 B83905 | hypothetical prote |
| 41 | 35 | 72.9 | 1012 | 2 I53172 | RAE-28 - mouse     |
| 42 | 35 | 72.9 | 1161 | 2 H95903 | probable chemotaxi |
| 43 | 35 | 72.9 | 1164 | 2 T03814 | tumor suppressor p |
| 44 | 34 | 70.8 | 110  | 2 C64598 | hypothetical prote |
| 45 | 34 | 70.8 | 229  | 2 T51587 | filamentous flower |

ALIGNMENTS

RESULT 1

ISZPT1

DNA topoisomerase (EC 5.99.1.2) - fission yeast (Schizosaccharomyces pombe)  
N:Alternate names: nicking-closing enzyme; omega-protein; relaxing enzyme; swivelase; ty  
C:Species: Schizosaccharomyces pombe  
C:Date: 30-Sep-1992 #sequence\_revision 30-Sep-1992 #text\_change 09-Jul-2004  
C:Accession: S03329  
R:Uemura, T.; Morino, K.; Uzawa, S.; Shiozaki, K.; Yanagida, M.  
Nucleic Acids Res. 15, 9727-9739, 1987  
A:Title: Cloning and sequencing of Schizosaccharomyces pombe DNA topoisomerase I gene,  
A:Reference number: S03329; MUID:88096534; PMID:2827111  
A:Accession: S03329  
A:Molecule type: DNA  
A:Residues: 1-812 <UEM>  
A:Cross-references: UNIPROT:P07799; EMBL:X06201; NID:G5118; PIDN:CAA29559.1; PID:G5119  
C:Comment: Type I DNA topoisomerase catalyzes the ATP-independent transient breakage of  
in another, followed by rejoining. This reaction will lead to the conversion of one to  
C:Genetics: 5/1; 36/3  
A:Introns: 5/1; 36/3  
C:Superfamily: eukaryotic type I DNA topoisomerase  
C:Keywords: DNA binding; DNA replication; heterotetramer; isomerase  
F:771/Active site: Tyr #status Predicted

Query Match 85.4%; Score 41; DB 1; Length 812;  
Best Local Similarity 87.5%; Pred. No. 26;  
Matches 7; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 SPVNLPPPE 8  
:|||||  
Db 221 NPVNLPPPE 228

RESULT 2

T50327

DNA topoisomerase I [imported] - fission yeast (Schizosaccharomyces pombe)  
C:Species: Schizosaccharomyces pombe  
C:Date: 09-Jun-2000 #sequence\_revision 09-Jun-2000 #text\_change 09-Jul-2004  
R:McDougall, R.C.; Rajadream, M.A.; Barrell, B.G.; Cadieu, E.; Lelaure, V.; Galibert, F.  
submitted to the EMBL Data Library, January 2000  
C:Accession: T50327  
A:Reference number: Z25061  
A:Accession: T50327  
A:Status: preliminary; translated from GB/EMBL/DBJ  
A:Molecule type: DNA  
A:Residues: 1-814 <MCD>  
A:Cross-references: UNIPROT:P07799; EMBL:AL136536; PIDN:CA566458.1; GSPDB:GNO0067; SPDB

A:Genetic: 5/1; 38/3  
A:Map position: 2  
A:Introns: 5/1; 38/3  
C:Superfamily: eukaryotic type I DNA topoisomerase



```

QY      1 SPVNLPPPEL 9
      || :|||||
Db      39 SPYDLPPPEL 47

RESULT 7
A43359
Microtubule-associated protein MAP1A - rat
C:Species: Rattus norvegicus (Norway rat)
C>Date: 31-Dec-1993 #sequence_revision 31-Dec-1993 #text_change 09-Jul-2004
C:Accession: A43359; S22108
R:Langkopf, A.; Hammarback, J.A.; Muller, R.; Vallee, R.B.; Garner, C.C.
J. Biol. Chem. 267, 16561-16566, 1992
A:Title: Microtubule-associated proteins 1A and 1C2. Two proteins encoded in one messenger RNA
A:Reference number: A43359; MUID:92355629; PMID:1379599
A:Accession: A43359
A:Molecule type: mRNA
A:Residues: 1-2774 <LAN>
A:Cross-references: UNIPROT:P34926; GB:M83196; NID:G205537; PIDN:AAB48069.1; PID:G205538
A>Note: sequence extracted from NCBI backbone (NCBI:111039, NCBI:P:111040)
R:Cravchik, A.
submitted to the EMBL Data Library, June 1992
A:Reference number: S22108
A:Accession: S22108
A>Status: preliminary
A:Molecule type: mRNA
A:Residues: 73-364, 'NRLRS', 370, 'QKN', 374, 'PSPKGL', 381-751, 'RSMMSQMNQARR', 764, 'D', 766, 'LR', 'WLRNMCPPQRRSP', 851, 'V', 853, 'NSL', 855, 'LPHRWLRTN', 865, 'W', 867, 'HSQLPDGDD', 877, 'Q', 879, '
A:Cross-references: EMBL:X66840
A:Experimental source: strain Sprague Dawley
C:Superfamily: microtubule-associated protein MAP1B
C:Keywords: microtubule binding; phosphoprotein

Query Match      79.2%; Score 38; DB 2; Length 2774;
Best Local Similarity 87.5%; Pred. No. 3.4e+02;
Matches 7; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      1 SPVNLPPPE 8
      ||| :|||||
Db      1742 SPVGLPPE 1749

RESULT 8
A99624
NADH dehydrogenase chain 1 ND1 [imported] - Casuarinus casuarinus mitochondrion
C:Species: mitochondrion Casuarinus casuarinus
C>Date: 15-Jun-2001 #sequence_revision 15-Jun-2001 #text_change 09-Jul-2004
C:Accession: A99624
R:Haddrath, O.; Baker, A.J.
Proc. R. Soc. Lond. B Biol. Sci. 268, 939-945, 2001
A:Title: Complete mitochondrial DNA genome sequences of extinct birds: ratite phylogene
A:Reference number: A99613; MUID:21263106; PMID:11370967
A:Accession: A99624
A>Status: preliminary
A:Molecule type: DNA
A:Residues: 1-323 <KUR>
A:Cross-references: UNIPROT:Q957Z5; GB:NC_002778; NID:G14141870; PIDN:NP_115350.1; GSPDB
C:Genetics:
A:Gene: ND1
A:Genome: mitochondrion
A:Genetic code: SGCI
C:Superfamily: NADH:quinone oxidoreductase (complex I), subunit 1/[NiFe]-hydrogenase-3-t
C:Keywords: mitochondrion

Query Match      77.1%; Score 37; DB 2; Length 323;
Best Local Similarity 77.8%; Pred. No. 47;
Matches 7; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY      1 SPVNLPPPEL 9
      || :|||||
Db      252 SSLNLPPPEL 260

RESULT 11
T11167
NADH2 dehydrogenase (ubiquinone) (EC 1.6.5.3) chain 1 - Greater rhea mitochondrion
C:Species: mitochondrion Rhea americana (greater rhea, common rhea)
C>Date: 16-Jul-1999 #sequence_revision 16-Jul-1999 #text_change 09-Jul-2004
C:Accession: T11167; T11416
R:Mindell, D.P.; Sorenson, M.D.; Dimcheff, D.E.
Proc. Natl. Acad. Sci. U.S.A. 95, 10693-10697, 1998
A:Title: Multiple independent origins of mitochondrial gene order in birds.
A:Reference number: 217242

```

```

RESULT 9
A99622
NADH dehydrogenase chain 1 ND1 [imported] - Anomalopteryx didiformis mitochondrion
C:Species: mitochondrion Anomalopteryx didiformis
C>Date: 15-Jun-2001 #sequence_revision 15-Jun-2001 #text_change 09-Jul-2004
C:Accession: A99622
R:Haddrath, O.; Baker, A.J.
Proc. R. Soc. Lond. B Biol. Sci. 268, 939-945, 2001
A:Title: Complete mitochondrial DNA genome sequences of extinct birds: ratite phylogen
A:Reference number: A99613; MUID:21263106; PMID:11370967
A:Accession: A99622
A>Status: preliminary
A:Molecule type: DNA
A:Residues: 1-323 <KUR>
A:Cross-references: UNIPROT:Q957V7; GB:NC_002779; NID:G14141926; PIDN:NP_115363.1; GSPDB
C:Genetics:
A:Gene: ND1
A:Genome: mitochondrion
A:Genetic code: SGCI
C:Superfamily: NADH:quinone oxidoreductase (complex I), subunit 1/[NiFe]-hydrogenase-3-t
C:Keywords: mitochondrion

Query Match      77.1%; Score 37; DB 2; Length 323;
Best Local Similarity 77.8%; Pred. No. 47;
Matches 7; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY      1 SPVNLPPPEL 9
      || :|||||
Db      252 SSLNLPPPEL 260

RESULT 10
A90616
NADH dehydrogenase chain 1 ND1 [imported] - Pterocnemia pennata mitochondrion
C:Species: mitochondrion Pterocnemia pennata
C>Date: 15-Jun-2001 #sequence_revision 15-Jun-2001 #text_change 09-Jul-2004
C:Accession: A90616
R:Haddrath, O.; Baker, A.J.
Proc. R. Soc. Lond. B Biol. Sci. 268, 939-945, 2001
A:Title: Complete mitochondrial DNA genome sequences of extinct birds: ratite phylogene
A:Reference number: A99613; MUID:21263106; PMID:11370967
A:Accession: A90616
A>Status: preliminary
A:Molecule type: DNA
A:Residues: 1-324 <KUR>
A:Cross-references: UNIPROT:Q95888; GB:NC_002783; NID:G14141898; PIDN:NP_115415.1; GSPDB
C:Genetics:
A:Gene: ND1
A:Genome: mitochondrion
A:Genetic code: SGCI
C:Superfamily: NADH:quinone oxidoreductase (complex I), subunit 1/[NiFe]-hydrogenase-3-t
C:Keywords: mitochondrion

Query Match      77.1%; Score 37; DB 2; Length 324;
Best Local Similarity 77.8%; Pred. No. 47;
Matches 7; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY      1 SPVNLPPPEL 9
      || :|||||
Db      252 SSLNLPPPEL 260

RESULT 11
T11167
NADH2 dehydrogenase (ubiquinone) (EC 1.6.5.3) chain 1 - Greater rhea mitochondrion
C:Species: mitochondrion Rhea americana (greater rhea, common rhea)
C>Date: 16-Jul-1999 #sequence_revision 16-Jul-1999 #text_change 09-Jul-2004
C:Accession: T11167; T11416
R:Mindell, D.P.; Sorenson, M.D.; Dimcheff, D.E.
Proc. Natl. Acad. Sci. U.S.A. 95, 10693-10697, 1998
A:Title: Multiple independent origins of mitochondrial gene order in birds.
A:Reference number: 217242

```

A;Accession: T11167  
 A;Status: preliminary; translated from GB/EMBL/DBJ  
 A;Molecule type: DNA  
 A;Residues: 1-324 <MIN>  
 A;Cross-references: UNIPROT:O79392; EMBL:AF090339; NID:g4894475; PID:g4894476; PIDN:AA03R;Harlid, A.  
 submitted to the EMBL Data Library, May 1999  
 A;Reference number: Z17270  
 A;Accession: T11416  
 A;Status: translated from GB/EMBL/DBJ  
 A;Molecule type: DNA  
 A;Residues: 1-284;P, 286-324 <HAR>  
 A;Cross-references: EMBL:Y16884; PIDN:CAA76501.2  
 C;Genetics:  
 A;Genome: mitochondrion  
 A;Genetic code: SCS1  
 C;Superfamily: NADH:quinone oxidoreductase (complex I), subunit 1/[NiFe]-hydrogenase-3-b  
 C;Keywords: membrane-associated complex; mitochondrion; NAD; oxidative phosphorylation;

Query Match 77.1%; Score 37; DB 2; Length 324;  
 Best Local Similarity 77.8%; Pred. No. 47;  
 Matches 7; Conservative 1; Mismatches 1; Indels 1; Gaps 0;

Qy 1 SPVNLPPPEL 9  
 | : |||||  
 Db 252 SSLNLPPPEL 260

RESULT 12  
 G96519  
 hypothetical protein T2J15.14 [imported] - Arabidopsis thaliana  
 C;Species: Arabidopsis thaliana (mouse-ear cress)  
 C;Date: 02-Mar-2001 #sequence\_revision 02-Mar-2001 #text\_change 09-Jul-2004  
 C;Accession: G96519  
 R;Theologos, A.; Ecker, J.R.; Palm, C.J.; Federspiel, N.A.; Kaul, S.; White, O.; Alonso,  
 Chin, C.W.; Chung, M.K.; Conn, L.; Conway, A.B.; Conway, A.R.; Creasy, T.H.; Dewar, K.;  
 ansen, N.F.; Hughes, B.; Huizar, L.  
 Nature 408, 816-820, 2000  
 A;Authors: Hunter, J.L.; Jenkins, J.; Johnson-Hopson, C.; Khan, S.; Khaykin, E.; Kim, C.  
 C.A.; Li, J.H.; Li, Y.; Lin, X.; Liu, S.X.; Liu, Z.A.; Luros, J.S.; Matti, R.; Marziani,  
 Rizzo, M.; Rooney, T.; Rowley, D.; Sakano, H.  
 A;Authors: Salzberg, S.L.; Schwartz, J.R.; Shinn, P.; Southwick, A.M.; Sun, H.; Tallon,  
 ker, M.; Wu, D.; Yu, G.; Fraser, C.M.; Venter, J.C.; Davis, R.W.  
 A;Title: Sequence and analysis of chromosome 1 of the plant Arabidopsis.  
 A;Reference number: A86141; MUID:21016719; PMID:11130712  
 A;Accession: G96519  
 A;Status: preliminary  
 A;Molecule type: DNA  
 A;Residues: 1-328 <STO>  
 A;Cross-references: UNIPROT:Q9C7Y7; GB:AE005173; NID:g10645466; PIDN:AAG21580.1; GSPDB:G  
 C;Genetics:  
 A;Gene: T2J15.14  
 A;Map position: 1

Query Match 77.1%; Score 37; DB 2; Length 328;  
 Best Local Similarity 66.7%; Pred. No. 48;  
 Matches 6; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

Qy 1 SPVNLPPPEL 9  
 | : |||||  
 Db 106 SPLNLPPPEL 114

## RESULT 13

G72235  
 hypothetical protein - Thermotoga maritima (strain MSB8)  
 C;Species: Thermotoga maritima  
 C;Date: 11-Jun-1999 #sequence\_revision 11-Jun-1999 #text\_change 09-Jul-2004  
 C;Accession: G72235  
 R;Nelson, K.E.; Clayton, R.A.; Gill, S.R.; Gwinn, M.L.; Dodson, R.J.; Haft, D.H.; Hickey  
 Garrett, M.M.; Stewart, A.M.; Cotton, M.D.; Pratt, M.S.; Phillips, C.A.; Richardson, D.;  
 C.M.  
 Nature 399, 323-329, 1999

A;Title: Evidence for lateral gene transfer between Archaea and Bacteria from genome seq  
 A;Reference number: A72200; MUID:99287316; PMID:10360571  
 A;Accession: G72235  
 A;Status: preliminary  
 A;Molecule type: DNA  
 A;Residues: 1-360 <ARN>  
 A;Cross-references: UNIPROT:Q9X1R9; GB:AE001803; GB:AE000512; NID:g4982150; PIDN:AA03665C  
 A;Experimental source: strain MSB8  
 C;Genetics:  
 A;Gene: TM1583  
 C;Superfamily: Thermotoga maritima hypothetical protein TM1583

Query Match 77.1%; Score 37; DB 2; Length 360;  
 Best Local Similarity 75.0%; Pred. No. 53;  
 Matches 6; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy 2 PVNLPPPEL 9  
 | : |||||  
 Db 171 PVSIPPEL 178

## RESULT 14

S58643  
 probable transcription factor SPT20 - yeast (Saccharomyces cerevisiae)  
 N;Alternate names: protein AOE555; protein O0452; protein YOL148c  
 C;Species: Saccharomyces cerevisiae  
 C;Date: 28-Oct-1995 #sequence\_revision 03-Nov-1995 #text\_change 09-Jul-2004  
 C;Accession: S58643; S60388; S66845; S57676  
 R;Roberts, S.M.; Winston, F.  
 submitted to the EMBL Data Library, March 1995  
 A;Reference number: S58643  
 A;Accession: S58643  
 A;Molecule type: DNA  
 A;Residues: 1-604 <ROB>  
 A;Cross-references: UNIPROT:P50875; EMBL:U22063; NID:g722280; PID:g722281  
 R;Casamayor, A.; Aldea, M.; Casas, C.; Herrero, E.; Gamo, F.J.; Lafuente, M.J.; Gancedo,  
 Yeast 11, 1281-1288, 1995  
 A;Title: DNA sequence analysis of a 13 kbp fragment of the left arm of yeast chromosome 1  
 A;Reference number: S60385; MUID:96132030; PMID:8553699  
 A;Accession: S60388  
 A;Status: nucleic acid sequence not shown  
 A;Molecule type: DNA  
 A;Residues: 50-292,'S',294-604 <CAS>  
 A;Cross-references: EMBL:248239; NID:g1163073; PIDN:CAA88279.1; PID:g886948  
 R;Arino, J.; Casamayor, A.; Gamo, F.J.; Gancedo, C.; Lafuente, M.J.; Aldea, M.; Casas, C.  
 submitted to the Protein Sequence Database, July 1996  
 A;Reference number: S66814  
 A;Accession: S66845  
 A;Molecule type: DNA  
 A;Residues: 1-604 <ARI>  
 A;Cross-references: EMBL:Z74890; NID:g1420051; PID:e252310; PID:g1420052; MIPS:YOL148C  
 A;Experimental source: strain S288C  
 C;Genetics:  
 A;Gene: SGD:SPT20; ADAS  
 A;Cross-references: SGD:S0005508; MIPS:YOL148C  
 A;Map position: 15L

Query Match 77.1%; Score 37; DB 2; Length 604;  
 Best Local Similarity 66.7%; Pred. No. 94;  
 Matches 6; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

Qy 1 SPVNLPPPEL 9  
 | : |||||  
 Db 30 SPVNVPPPM 38

## RESULT 15

H81982  
 hypothetical protein NMA0631 [imported] - Neisseria meningitidis (strain Z2491 serogroup  
 C;Species: Neisseria meningitidis  
 C;Date: 05-May-2000 #sequence\_revision 05-May-2000 #text\_change 09-Jul-2004  
 C;Accession: H81982  
 R;Parkhill, J.; Achtman, M.; James, K.D.; Bentley, S.D.; Churcher, C.; Klee, S.R.; Morel]



; Holroyd, S.; Jagels, K.; Leather, S.; Moule, S.; Mungall, K.; Quail, M.A.; Rajandream,  
Nature 404, 502-506, 2000  
A:Title: Complete DNA sequence of a serogroup A strain of *Neisseria meningitidis* Z2491.  
A:Reference number: A81775; MUID:20222556; PMID:10761919  
A:Accession: H81982  
A:Status: preliminary  
A:Molecule type: DNA  
A:Residues: 1-1082 <PAR>  
A:Cross-references: UNIPROT:Q9JVX9; GB:AL162753; GB:AL157959; NID:g7379120; PIDN:CAB8392  
A:Experimental source: serogroup A, strain Z2491  
C:Genetics:  
A:Gene: NMA0631  
C:Superfamily: *Neisseria meningitidis* hypothetical protein NMA0631

Query Match 77.1%; Score 37; DB 2; Length 1082;  
Best Local Similarity 77.8%; Pred. No. 1.8e+02;  
Matches 7; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 SPVNLPPPEL 9  
||:|||||  
DB 370 SPLNLSPEL 378

Search completed: November 19, 2004, 23:44:58  
Job time : 8.29577 secs

**This Page Blank (uspto)**

GenCore version 5.1.6  
Copyright (c) 1993 - 2004 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: November 19, 2004, 23:32:13 ; Search time 32.1972 Seconds  
(without alignments)  
160.833 Million cell updates/sec

Title: US-10-068-725-4\_COPY\_110\_118  
Perfect score: 48  
Sequence: 1 SPVNLPPPEL 9

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 1825181 seqs, 575374646 residues

Total number of hits satisfying chosen parameters: 1825181

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000  
Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : Uniprot\_02: \*  
1: uniprot\_sprot: \*  
2: uniprot\_trembl: \*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Score | Query Match | Length | DB ID | Description |
|------------|-------|-------------|--------|-------|-------------|
| 1          | 48    | 100.0       | 247    | 2     | Q726F5      |
| 2          | 48    | 100.0       | 293    | 1     | T13X_HUMAN  |
| 3          | 41    | 85.4        | 814    | 1     | TOPI_SCHPO  |
| 4          | 41    | 85.4        | 1289   | 2     | Q7RK2       |
| 5          | 40    | 83.3        | 778    | 1     | TOPI_CANAL  |
| 6          | 40    | 83.3        | 1011   | 2     | Q93882      |
| 7          | 40    | 83.3        | 1044   | 2     | Q6M9G4      |
| 8          | 40    | 83.3        | 1044   | 2     | CAF05993    |
| 9          | 39    | 81.2        | 62     | 2     | Q6Q228      |
| 10         | 39    | 81.2        | 62     | 2     | AAS90616    |
| 11         | 39    | 81.2        | 292    | 2     | Q82X60      |
| 12         | 39    | 81.2        | 330    | 2     | Q89QS3      |
| 13         | 39    | 81.2        | 854    | 2     | Q9FVG6      |
| 14         | 39    | 81.2        | 905    | 1     | SNF5_YEAST  |
| 15         | 39    | 81.2        | 1124   | 2     | Q9CM76      |
| 16         | 38    | 79.2        | 261    | 2     | Q7U5L2      |
| 17         | 38    | 79.2        | 276    | 2     | Q7QXT8      |
| 18         | 38    | 79.2        | 381    | 2     | Q7VTR0      |
| 19         | 38    | 79.2        | 381    | 2     | Q7W2A3      |
| 20         | 38    | 79.2        | 381    | 2     | Q7WR70      |
| 21         | 38    | 79.2        | 384    | 1     | H182_ANASP  |
| 22         | 38    | 79.2        | 389    | 2     | Q725T0      |
| 23         | 38    | 79.2        | 389    | 2     | AAS97813    |
| 24         | 38    | 79.2        | 447    | 2     | Q8RPM1      |
| 25         | 38    | 79.2        | 536    | 2     | Q89VVS      |
| 26         | 38    | 79.2        | 563    | 2     | Q8BI72      |
| 27         | 38    | 79.2        | 564    | 2     | Q7XA49      |
| 28         | 38    | 79.2        | 579    | 2     | Q8TBM5      |
| 29         | 38    | 79.2        | 580    | 2     | Q9NXV6      |
| 30         | 38    | 79.2        | 581    | 2     | Q7V7K8      |
| 31         | 38    | 79.2        | 631    | 2     | Q9NYH0      |

|    |    |      |      |   |            |
|----|----|------|------|---|------------|
| 32 | 38 | 79.2 | 703  | 2 | Q9ST08     |
| 33 | 38 | 79.2 | 751  | 2 | Q888J6     |
| 34 | 38 | 79.2 | 992  | 2 | Q8L499     |
| 35 | 38 | 79.2 | 1085 | 2 | Q755J0     |
| 36 | 38 | 79.2 | 1085 | 2 | AAS53207   |
| 37 | 38 | 79.2 | 1089 | 2 | Q9FN97     |
| 38 | 38 | 79.2 | 1153 | 2 | Q8S0G6     |
| 39 | 38 | 79.2 | 2774 | 1 | MAPA_RAT   |
| 40 | 38 | 79.2 | 2805 | 1 | MAPA_HUMAN |
| 41 | 37 | 77.1 | 68   | 2 | Q7OUU3     |
| 42 | 37 | 77.1 | 68   | 2 | CAD60951   |
| 43 | 37 | 77.1 | 299  | 2 | Q7NEJ4     |
| 44 | 37 | 77.1 | 323  | 2 | Q9B6X0     |
| 45 | 37 | 77.1 | 323  | 2 | Q9B6Z3     |

ALIGNMENTS

RESULT 1

Q726F5 PRELIMINARY; PRT; 247 AA.  
AC Q726F5;  
DT 01-OCT-2003 (TrEMBLrel. 25, Created)  
DT 01-OCT-2003 (TrEMBLrel. 25, Last sequence update)  
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)  
DE Transmembrane activator and CAML interactor.  
GN Name=TNFRSF13B;  
OS Homo sapiens (Human).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
OX NCBI\_TaxID=9606;  
RN [1]  
RP SEQUENCE FROM N.A.  
RA Zhou G., Ke R., Li H., Zheng G., Shen C., Lin L., Yang S.;  
RL Submitted (MAY-2003) to the EMBL/GenBank/DBSJ databases.  
DR EMBL; AY302137; AAP57629.1; -;  
KW GO; GO:0016021; C:integral to membrane; IEA.  
KW Transmembrane.  
SQ SEQUENCE 247 AA; 26664 MW; 850E1F4C2578B8E6 CRC64;

Query Match 100.0%; Score 48; DB 2; Length 247;  
Best Local Similarity 100.0%; Pred. No. 2.6;  
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SPVNLPPPEL 9  
Db 64 SPVNLPPPEL 72

RESULT 2

T13X\_HUMAN STANDARD; PRT; 293 AA.  
ID T13X\_HUMAN  
AC O14836;  
DT 28-FEB-2003 (Rel. 41, Created)  
DT 28-FEB-2003 (Rel. 41, Last sequence update)  
DT 05-JUL-2004 (Rel. 44, Last annotation update)  
DE Tumor necrosis factor receptor superfamily member 13B (Transmembrane activator and CAML interactor).  
GN Name=TNFRSF13B; Synonyms=TACI;  
OS Homo sapiens (Human).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
OX NCBI\_TaxID=9606;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC TISSUE=B-cell;  
RX MEDLINE=97458245; PubMed=9311921;  
RA von Buelow G.-U., Bram R.J.;  
RT "NF-AT activation induced by a CAML-interacting member of the tumor necrosis factor receptor superfamily.";  
RL Science 278:138-141(1997). [2]

SEQUENCE FROM N.A.  
RC TISSUE=Blood;  
RX MEDLINE=2238257; PubMed=12477932; DOI=10.1073/pnas.242603899;  
RA Strausberg R.L., Feingold E.A., Grouse L.H., Berge J.G.,  
RA Klausner R.D., Collins F.S., Wagner L., Sherman C.M., Schuler G.D.,  
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,  
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,  
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,  
RA Stapleton M., Soares M.B., Bonaldo M.P., Casavant T.L., Scheetz T.E.,  
RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,  
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullany S.J.,  
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,  
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,  
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,  
RA Fahey J., Helton E., Kettman M., Madan A., Rodrigues S., Sanchez A.,  
RA Whiting J., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,  
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,  
RA Rodriguez A.C., Grinwood J.J., Schmutz J., Myers R.M.,  
RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smallos D.E.,  
RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.,  
RA "Generation and initial analysis of more than 15,000 full-length human  
RT and mouse cDNA sequences.";  
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).  
RN [3]  
RP FUNCTION.  
RX MEDLINE=20519647; PubMed=10956646; DOI=10.1074/jbc.M005224200;  
RA Wu Y., Bressette D., Carrell J.A., Kaufman T., Feng P., Taylor K.,  
RA Gan Y., Cho Y.H., Garcia A.D., Gollatz E., Dimke D., Lafleur D.,  
RA Migone T.S., Nardelli B., Wei P., Ruben S.M., Ullrich S.J.,  
RA Olsen H.S., Kanakara P., Moore P.A., Baker K.P.;  
RT "Tumor necrosis factor (TNF) receptor superfamily member TACI is a  
RT high affinity receptor for TNF family members APRIL and BlyS.";  
RL J. Biol. Chem. 275:35478-35485(2000).  
RN [4]  
RP FUNCTION.  
RX MEDLINE=21170294; PubMed=10973284; DOI=10.1038/79802;  
RA Yu G., Boone T., Delaney J., Hawkins N., Kelley M., Ramakrishnan M.,  
RA McCabe S., Qiu W.R., Kornuc M., Xia X.-Z., Guo J., Stolina M.,  
RA Boyle W.J., Sarosi I., Hsu H., Senaldi G., Theill L.E.;  
RT "APRIL and TALL-1 and receptors BCMA and TACI: system for regulating  
RT humoral immunity.";  
RL Nat. Immunol. 1:252-256(2000).  
RN [5]  
RP INTERACTIONS WITH TRAF2 AND TRAF5.  
RX MEDLINE=20341628; PubMed=10880535;  
RA Xia X.-Z., Treanor J., Senaldi G., Khare S.D., Boone T., Kelley M.,  
RA Theill L.E., Colombero A., Solovyev I., Lee F., McCabe S., Elliott R.,  
RA Miner K., Hawkins N., Guo J., Stolina M., Yu G., Wang J., Delaney J.,  
RA Meng S.Y., Boyle W.J., Hsu H.;  
RT "TACI is a TRAF-interacting receptor for TALL-1, a tumor necrosis  
RT factor family member involved in B cell regulation.";  
RL J. Exp. Med. 192:137-143(2000).  
CC -1- FUNCTION: Receptor for TNFSF13/APRIL and TNFSF13B/TALL1/BAPF/BLYS  
CC that binds both ligands with similar high affinity. Mediates  
CC calcineurin-dependent activation of NF-AT, as well as activation  
CC of NF-kappa-B and AP-1. Involved in the stimulation of B- and T-  
CC cell function and the regulation of humoral immunity.  
CC -1- SUBUNIT: Binds TRAF2, TRAF5 and TRAF6. Binds the NH2-terminal  
CC domain of CAMLg with its C-terminus.  
CC -1- SUBCELLULAR LOCATION: Type III membrane protein.  
CC -1- TISSUE SPECIFICITY: Highly expressed in spleen, thymus, small  
CC intestine and peripheral blood leukocytes. Expressed in resting B-  
CC cells and activated T-cells, but not in resting T-cells.  
CC -1- SIMILARITY: Contains 2 TNFR-Cys repeats.  
CC -1- CAUTION: It is uncertain whether Met-1 or Met-31 is the initiator.  
CC This SWISS-PROT entry is copyright. It is produced through a collaboration  
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -  
CC the European Bioinformatics Institute. There are no restrictions on its  
CC use by non-profit institutions as long as its content is in no way  
CC modified and this statement is not removed. Usage by and for commercial  
CC entities requires a license agreement (see <http://www.ebi.ac.uk/announcements/>  
CC or send an email to [license@ebi.ac.uk](mailto:license@ebi.ac.uk)).

CC -----  
DR EMBL; AF023614; AAC51790.1; -;  
DR EMBL; BC028072; AAH28072.1; -;  
DR HSPG; Q9Y275; IQDD.  
DR Genew; HGNC:18153; TNFRSF13B.  
DR MIM; 604907; -;  
DR GO; GO:0005887; C-integral to plasma membrane; TAS.  
DR GO; GO:0004872; F:receptor activity; TAS.  
DR GO; GO:0007166; P:cell surface receptor linked signal transdu. .; TAS.  
DR InterPro; IPR001368; TNFR C6.  
DR PROSITE; PS00652; TNFR NGFR 1; 1.  
DR PROSITE; PS00050; TNFR NGFR 2; FALSE NEG.  
KW Glycoprotein; Immune response; Receptor; Repeat; Signal-anchor;  
KW Transmembrane.  
FT DOMAIN 1 165 Extracellular (Potential).  
FT DOMAIN 166 186 Signal-anchor for type III membrane  
FT DOMAIN 187 293 Cytoplasmic (Potential).  
FT REPEAT 33 67 TNFR-Cys 1.  
FT REPEAT 70 104 TNFR-Cys 2.  
FT DISULFID 34 47 By similarity.  
FT DISULFID 50 62 By similarity.  
FT DISULFID 54 66 By similarity.  
FT DISULFID 71 86 By similarity.  
FT DISULFID 89 100 By similarity.  
FT DISULFID 93 104 By similarity.  
FT CARBOHYD 128 128 N-linked (GlcNAc...) (Potential).  
FT CONFLICT 251 251 P -> L (in Ref. 2).  
SQ SEQUENCE 293 AA; 31816 MW; 411799F3DE17A5EB CRC64;  
Query Match 100.0%; Score 48; DB 1; Length 293;  
Best Local Similarity 100.0%; Pred. No. 3.1;  
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 SPVNLPEEL 9  
DB 110 SPVNLPEEL 118  
RESULT 3  
TOP1 SCHPO STANDARD; PRT; 814 AA.  
AC P07739; Q9P7V7;  
DT 01-AUG-1988 (Rel. 08, Created)  
DT 16-OCT-2001 (Rel. 40, Last sequence update)  
DE 05-JUL-2004 (Rel. 44, Last annotation update)  
DE DNA topoisomerase I (EC 5.99.1.2).  
GN Name=TopI; ORFNames=SPC1703.14C;  
OS Schizosaccharomyces pombe (Fission Yeast).  
OC Eukaryota; Fungi; Ascomycota; Schizosaccharomycetes;  
OC Schizosaccharomycetales; Schizosaccharomycetaceae;  
OC Schizosaccharomycetes.  
OX NCBI\_TaxID=4896;  
RN [1]  
RP SEQUENCE FROM N.A.  
RX STRAIN=972;  
RX MEDLINE=88096534; PubMed=2827111;  
RA Uemura T., Morino K., Uzawa S., Shiozaki K., Yanagida M.;  
RT "Cloning and sequencing of Schizosaccharomycetes pombe DNA topoisomerase  
RT I gene, and effect of gene disruption.";  
RL Nucleic Acids Res. 15:9727-9739(1987).  
RN [2]  
RP SEQUENCE FROM N.A.  
RX STRAIN=972;  
RX MEDLINE=21848401; PubMed=11859360; DOI=10.1038/nature724;  
RA Wood V., Gwilliam R., Rajandream M.A., Lyne M., Lyne R., Stewart A.,  
RA Scouras J., Peat N., Hayles J., Baker S., Basham D., Bowman S.,  
RA Brooks K., Brown D., Brown S., Chillingworth T., Churcher C.M.,  
RA Collins M., Connor R., Cronin A., Davis P., Fellwell T., Fraser A.,  
RA Gentles S., Goble A., Hamlin N., Harris D., Hidaigo J., Hodgson G.,  
RA Holroyd S., Hornsby T., Howarth S., Rucke E.J., Hunt S., Jagels K.,  
RA James K., Jones L., Jones M., Leather S., McDonald S., McLean J.,  
RA Mooney P., Moule S., Mungall K., Murphy L., Niblett D., Odell C.,

RA Oliver K., O'Neil S., Pearson D., Quail M.A., Rabinowitsch E.,  
 RA Rutherford J.K., Rutter S., Saunders D., Seeger K., Sharp S.,  
 RA Skelton J., Simmonds M., Squares R., Squares S., Stevens K.,  
 RA Taylor K., Taylor R.G., Tivey A., Walsh S.V., Warren T., Whitehead S.,  
 RA Woodward J., Volckaert G., Aert R., Robben J., Grymonprez B.,  
 RA Welljens I., Vanstreels E., Rieger M., Schaefer M., Mueller-Auer S.,  
 RA Gabel C., Fuchs M., Fritzc C., Holzer E., Moestl D., Hilbert H.,  
 RA Borzym K., Langer I., Beck A., Lehrach H., Wambutt R., Pohl T.M.,  
 RA Eger P., Zimmermann W., Wedler H., Gloubt S., Lelaure V., Mottier S.,  
 RA Goffeau A., Cadieu E., Dreano S., Gloubt S., Lelaure V., Mottier S.,  
 RA Galibert F., Aves S.J., Xiang Z., Hunt C., Moore K., Hurst S.M.,  
 RA Lucas M., Rochet M., Gaillardin C., Tallada V.A., Garzon A., Thode G.,  
 RA Daga R.R., Cruzado L., Jimenez J., Sanchez M., del Rey F., Benito J.,  
 RA Dominguez A., Revuelta J.L., Moreno S., Armstrong J., Forsburg S.L.,  
 RA Cerutti L., Lowe T., McCombie W.R., Paulsen I., Potashkin J.,  
 RA Shpakowski G.V., Usery D., Barrell B.G., Nurse P.;  
 RT "The genome sequence of Schizosaccharomyces pombe.";  
 RL Nature 415:871-880 (2002).  
 RN [3]  
 RP ACTIVE SITE TYROSINE.  
 RX MEDLINE=89340401; PubMed=2547758;  
 RA Eng W.-K., Pandit S.D., Sternglanz R.;  
 RT "Mapping of the active site tyrosine of eukaryotic DNA topoisomerase  
 I.";  
 RL J. Biol. Chem. 264:13373-13376(1989).  
 CC -|- FUNCTION: The reaction catalyzed by topoisomerases leads to the  
 CC conversion of one topological isomer of DNA to another.  
 CC -|- CATALYTIC ACTIVITY: ATP-independent breakage of single-stranded  
 CC DNA, followed by passage and rejoining.  
 CC -|- SUBUNIT: Monomer.  
 CC -|- MISCELLANEOUS: Eukaryotic topoisomerase I and II can relax both  
 CC negative and positive supercoils, whereas prokaryotic enzymes  
 CC relax only negative supercoils.  
 CC -|- MISCELLANEOUS: When a topoisomerase transiently breaks a DNA  
 CC backbone bond, it simultaneously forms a protein-DNA link, in  
 CC which a tyrosyl oxygen in the enzyme is joined to a DNA phosphorus  
 CC at one end of the enzyme-severed DNA strand.  
 CC -|- SIMILARITY: Belongs to the eukaryotic type I topoisomerase family.  
 CC  
 CC This SWISS-PROT entry is copyright. It is produced through a collaboration  
 CC between the Swiss Institute of Bioinformatics and the EMBL outstation -  
 CC the European Bioinformatics Institute. There are no restrictions on its  
 CC use by non-profit institutions as long as its content is in no way  
 CC modified and this statement is not removed. Usage by and for commercial  
 CC entities requires a license agreement (See <http://www.isb-sib.ch/announcement/>  
 CC or send an email to [license@isb-sib.ch](mailto:license@isb-sib.ch)).  
 CC -----  
 DR EMBL; X06201; CAA29559.1; -;  
 DR EMBL; AL136536; CAB66458.1; -;  
 DR PIR; S03329; ISZPT1.  
 DR PIR; T50327; T50327.  
 DR HSPR; P04786; 101S.  
 DR GeneDB\_SPombe; SPBC1703.14c; -;  
 DR InterPro; IPR011010; DNA\_brk\_join enz.  
 DR InterPro; IPR001631; Topoisomerase I.  
 DR InterPro; IPR009054; Topoisomerase Insert.  
 DR InterPro; IPR008336; Topoisomerase\_I\_N.  
 DR Pfam; PF01028; Topoisom\_I\_1.  
 DR Pfam; PF02919; Topoisom\_I\_N; 1.  
 DR PRINTS; PR00416; EUTPI5MRASE1.  
 DR SMART; SM00435; TOPEUC; 1.  
 DR PROSITE; PS00176; TOPOISOMERASE\_I\_EUK; 1.  
 KW DNA-binding; Isomerase; Topoisomerase.  
 FT ACT SITE 773 773 DNA cleavage.  
 FT CONFLICT 7 8 Missing (in Ref. 1).  
 FT CONFLICT 308 308 Q -> E (in Ref. 1).  
 FT CONFLICT 446 446 S -> N (in Ref. 1).  
 FT CONFLICT 698 698 V -> M (in Ref. 1).  
 SQ SEQUENCE 814 AA; 93980 MW; 842D8D81C92CE0A3 CRC64;  
 Query Match 85.4%; Score 41; DB 1; Length 814;  
 Best Local Similarity 87.5%; Pred. No. 1.6e+02;  
 Matches 7; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

```

Qy      1 SPVNLPPPE 8
Db      223 NPNVNLPPPE 230

RESULT 4
Q7RKA2
ID      Q7RKA2      PRELIMINARY;      PRT;      1289 AA.
AC      Q7RKA2;
DT      01-MAR-2004 (TtEMBLrel. 26, Created)
DT      01-MAR-2004 (TtEMBLrel. 26, Last sequence update)
DT      01-MAR-2004 (TtEMBLrel. 26, Last annotation update)
DE      Guanlyl cyclase enzyme-related (Fragment).
Name=PI02999;
OS      Plasmodium yoellii yoellii.
OC      Eukaryota; Alveolata; Apicomplexa; Haemosporida; Plasmodium.
NCBI_TaxID=73239;
[1]
RN      SEQUENCE FROM N.A.
RP
RC      STRAIN=17XNL;
RX      PubMed=12368865;
RA      Carlton J.M., Angiuoli S.V., Suh B.B., Koij T.W., Pertea M.,
RA      Silva J.C., Ermolaeva M.D., Allen J.E., Selengut J.D., Koo H.L.,
RA      Peterson J.D., Pop M., Kosack D.S., Shumway M.F., Bidwell S.L.,
RA      Shallow S.J., van Aken S.B., Riedmuller S.B., Feldblyum T.V.,
RA      Cho J.K., Quackenbush J., Sedegah M., Shoaihi A., Cummings L.M.,
RA      Florens L., Yates F.R. III, Raine J.D., Sinden R.E., Harris M.A.,
RA      Cunningham D.A., Preiser P.R., Bergman L.W., Vaidya A.B.,
RA      van Lin L.H., Janse C.J., Waters A.P., Smith H.O., White O.R.,
RA      Salzberg S.L., Venter J.C., Fraser C.M., Hoffman S.L., Gardner M.J.,
RA      Carucci D.J.;
RT      "genome sequence and comparative analysis of the model rodent malaria
RT      parasite Plasmodium yoellii yoellii.";
RL      Nature 419:512-519(2002).
CC      -I- CAUTION: The sequence shown here is derived from an
CC      EMBL/GenBank/DBJ whole genome shotgun (WGS) entry which is
CC      preliminary data.
DR      EMBL; ABRL0100846; EAA22522.1; -.
DR      GO; GO:0004383; F:guanylate cyclase activity; IEA.
DR      GO; GO:0016829; P:lyase activity; IEA.
DR      GO; GO:0007242; P:intracellular signaling cascade; IEA.
DR      InterPro; IPR001054; G cyclase.
DR      InterPro; IPR000504; RNA rec mot.
DR      Pfam; PF00211; Guanylate_cycf_2.
DR      PROSITE; PSS0125; GUANYLATE_CYCLASES_2; 2
DR      PROSITE; PSS00030; RRM_RNP_1; UNKNOWN_1.
KW      Lyase.
FT      NON TER
FT      1
SQ      SEQUENCE      1289 AA;      153106 MW;      DD2376AA8D3A199A CRC64;

Query Match      85.4%;      Score 41;      DB 2;      Length 1289;
Best Local Similarity      66.7%;      Pred. No. 2.7e+02;
Matches      6;      Conservative      3;      Mismatches      0;      Indels      0;      Gaps      0;

Qy      1 SPVNLPPPEL 9
Db      224 SPVNLPPPKI 232
||:||||:|

RESULT 5
TOPI CANAL
ID      TOPI CANAL      STANDARD;      PRT;      778 AA.
AC      Q00313; P78593;
DT      01-NOV-1997 (Rel. 35, Created)
DT      01-NOV-1997 (Rel. 35, Last sequence update)
DT      05-JUL-2004 (Rel. 44, Last annotation update)
DE      DNA topoisomerase I (EC 5.99.1.2).
Name=TOPI;
OS      Candida albicans (Yeast).
OC      Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
OC      Saccharomycetales; mitosporic Saccharomycetales; Candida.
NCBI_TaxID=5476;

```

RN SEQUENCE FROM N.A.  
 RC STRAIN-ATCC 10321 / CCM 8215;  
 RX MEDLINE=96242310; PubMed=9026437;  
 RA Taylor A., Giles K., Sarthy A.V., McGonigal T., Postel J.;  
 RT "Identification of the gene encoding DNA topoisomerase I from *Candida albicans*.";  
 RL FEMS Microbiol. Lett. 138:113-121 (1996).  
 RN [2]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=97195784; PubMed=90431115;  
 RA Jiang W., Gerhold D., Kniec E.B., Hauser M., Becker J.M., Koltin Y.;  
 RT "The topoisomerase I gene from *Candida albicans*.";  
 RL Microbiology 143:377-386 (1997).  
 CC -1- FUNCTION: The reaction catalyzed by topoisomerases leads to the  
 CC conversion of one topological isomer of DNA to another.  
 CC -1- CATALYTIC ACTIVITY: ATP-independent breakage of single-stranded  
 CC DNA, followed by passage and rejoining.  
 CC -1- MISCELLANEOUS: Eukaryotic topoisomerase I and II can relax both  
 CC negative and positive supercoils, whereas prokaryotic enzymes  
 CC relax only negative supercoils.  
 CC -1- MISCELLANEOUS: When a topoisomerase transiently breaks a DNA  
 CC backbone bond, it simultaneously forms a protein-DNA link, in  
 CC which a tyrosyl oxygen in the enzyme is joined to a DNA phosphorus  
 CC at one end of the enzyme-severed DNA strand.  
 CC -1- SIMILARITY: Belongs to the eukaryotic type I topoisomerase family.  
 CC  
 CC This SWISS-PROT entry is copyright. It is produced through a collaboration  
 CC between the Swiss Institute of Bioinformatics and the EMBL outstation -  
 CC the European Bioinformatics Institute. There are no restrictions on its  
 CC use by non-profit institutions as long as its content is in no way  
 CC modified and this statement is not removed. Usage by and for commercial  
 CC entities requires a license agreement (See <http://www.isb-sib.ch/announce/>  
 CC or send an email to [license@isb-sib.ch](mailto:license@isb-sib.ch)).  
 CC  
 CC -----  
 DR EMBL; U40454; AAC49381.1; -.  
 DR EMBL; U41342; AAB39507.1; -.  
 DR HSP; P04786; 101S.  
 DR InterPro; IPR011010; DNA\_brk\_join\_enz.  
 DR InterPro; IPR001631; Topoisomerase I.  
 DR InterPro; IPR008336; Topoisomerase I\_N.  
 DR Pfam; PF01028; Topoisom I; 1.  
 DR Pfam; PF02919; Topoisom I; 1.  
 DR PRINTS; PR00416; EUTPISMRASEI.  
 DR SMART; SM00435; TOPEUC; 1.  
 DR PROSITE; PS00176; TOPOISOMERASE\_I\_EUK; 1.  
 KW DNA-binding; Isomerase; Topoisomerase.  
 FT ACT\_SITE 736 736  
 FT CONFLICT 2 2 N -> S (in Ref. 2).  
 FT CONFLICT 61 61 K -> KRK (in Ref. 2).  
 FT CONFLICT 465 465 L -> F (in Ref. 2).  
 FT CONFLICT 623 623 I -> L (in Ref. 2).  
 FT CONFLICT 710 710 R -> K (in Ref. 2).  
 SQ SEQUENCE 778 AA; 90484 MW; BFABE6B22EA2E5D3 CRC64;  
  
 Query Match 83.3%; Score 40; DB 1; Length 778;  
 Best Local Similarity 100.0%; Pred. No. 2.3e+02;  
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
  
 QY 2 PVNLPPE 8  
 DB 186 PVNLPPE 192  
 |||||  
 |||||  
  
 RESULT 6  
 O93882 PRELIMINARY; PRT; 1011 AA.  
 AC O93882  
 DT 01-MAY-1999 (TrEMBLrel. 10, Created)  
 DT 01-MAY-1999 (TrEMBLrel. 10, Last sequence update)  
 DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)  
 DE TOL.  
 GN Name=tol;  
 OS Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes;

OS Neurospora crassa.  
 OC Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes;  
 OC Sordariomycetidae; Sordariales; Sordariaceae; Neurospora.  
 OX NCBI\_TaxID=5141;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=99126425; PubMed=9927450;  
 RA Shiu P.K.T., Glass N.L.;  
 RT "Molecular characterization of *tol*, a mediator of mating-type-  
 RT associated vegetative incompatibility in *Neurospora crassa*.";  
 RL Genetics 151:545-555 (1999).  
 DR EMBL; AF085183; AAC64945.1; -.  
 DR PIR; T17430; T17430.  
 DR InterPro; IPR010730; HET.  
 DR Pfam; PF06985; HET; 1.  
 SQ SEQUENCE 1011 AA; 113718 MW; EC1B7C5187F73FE7 CRC64;  
  
 Query Match 83.3%; Score 40; DB 2; Length 1011;  
 Best Local Similarity 66.7%; Pred. No. 3.1e+02;  
 Matches 6; Conservative 2; Mismatches 1; Indels 0; Gaps 0;  
  
 QY 1 SPVNLPPPEL 9  
 DB 85 SPINIPPHL 93  
 ||:|:|  
 ||:|:|  
  
 RESULT 7  
 Q6M9G4 PRELIMINARY; PRT; 1044 AA.  
 AC Q6M9G4  
 DT 05-JUL-2004 (TrEMBLrel. 27, Created)  
 DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)  
 DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)  
 DE Protein TOL.  
 GN Name=G21B4.080;  
 OS Neurospora crassa.  
 OC Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes;  
 OC Sordariomycetidae; Sordariales; Sordariaceae; Neurospora.  
 OX NCBI\_TaxID=5141;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RA Schulte U., Aign V., Hoheisel J., Brandt P., Fartmann B., Holland R.,  
 RA Nyakatura G., Mewes H.W., Mannhaupt G.;  
 RL Submitted (JAN-2004) to the EMBL/GenBank/DBJ databases.  
 RN [2]  
 RP SEQUENCE FROM N.A.  
 RA German Neurospora genome project;  
 RL Submitted (JAN-2004) to the EMBL/GenBank/DBJ databases.  
 DR EMBL; BX908808; CAF05993.1; -.  
 DR InterPro; IPR010730; HET.  
 DR Pfam; PF06985; HET; 1.  
 SQ SEQUENCE 1044 AA; 117616 MW; EB1DCE2AFC41F287 CRC64;  
  
 Query Match 83.3%; Score 40; DB 2; Length 1044;  
 Best Local Similarity 66.7%; Pred. No. 3.2e+02;  
 Matches 6; Conservative 2; Mismatches 1; Indels 0; Gaps 0;  
  
 QY 1 SPVNLPPPEL 9  
 DB 85 SPINIPPHL 93  
 ||:|:|  
 ||:|:|  
  
 RESULT 8  
 CAF05993 PRELIMINARY; PRT; 1044 AA.  
 ID CAF05993  
 AC CAF05993  
 DT 02-MAR-2004 (TrEMBLrel. 27, Created)  
 DT 02-MAR-2004 (TrEMBLrel. 27, Last sequence update)  
 DT 02-MAR-2004 (TrEMBLrel. 27, Last annotation update)  
 DE Protein TOL.  
 GN G21B4.080.  
 OS Neurospora crassa.  
 OC Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes;

OC Sordariomycetidae; Sordariales; Sordariaceae; Neurospora.  
 OX NCBI\_TaxID=5141;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RA Schulte U., Aign V., Hoheisel J., Brandt P., Fartmann B., Holland R.,  
 RA Nyakatura G., Mewes H.W., Mannhaupt G.;  
 RL Submitted (JAN-2004) to the EMBL/GenBank/DBJ databases.  
 RN [2]  
 RP SEQUENCE FROM N.A.  
 RA German Neurospora genome project;  
 RL Submitted (JAN-2004) to the EMBL/GenBank/DBJ databases.  
 DR EMBL; BX90808; CAF05993.1; -;  
 SQ SEQUENCE 1044 AA; 117616 MW; B81DCE2AFC41F287 CRC64;

Query Match 83.3%; Score 40; DB 2; Length 1044;  
 Best Local Similarity 66.7%; Pred. No. 3.2e+02;  
 Matches 6; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 SPVNLPPPEL 9  
 ||:|||||  
 DB 85 SPINIPPHL 93

## RESULT 9

Q6Q228 PRELIMINARY; PRT; 62 AA.  
 ID Q6Q228;  
 AC Q6Q228;  
 DT 05-JUL-2004 (TrEMBLrel. 27, Created)  
 DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)  
 DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)  
 DE Putative glucosamine-fructose-6-phosphate aminotransferase  
 DE (Fragment).  
 OS uncultured soil bacterium.  
 OC Bacteria; environmental samples.  
 OX NCBI\_TaxID=164851;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RA Riesenfeld C.S., Goodman R.M., Handelsman J.;  
 RL Submitted (MAR-2004) to the EMBL/GenBank/DBJ databases.  
 DR EMBL; AY566824; AAS90616.1; -;  
 DR GO; GO:0008483; F:transaminase activity; IEA.  
 DR GO; GO:0016740; F:transferase activity; IEA.  
 KW Amino transferase; Transferase.  
 FT NON\_TER 1  
 SQ SEQUENCE 62 AA; 6835 MW; 4BFCBC9E94F35A4E CRC64;

Query Match 81.2%; Score 39; DB 2; Length 62;  
 Best Local Similarity 66.7%; Pred. No. 22;  
 Matches 6; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 SPVNLPPPEL 9  
 ||:|||||  
 DB 13 SPIQLPPEI 21

## RESULT 10

AAS90616 PRELIMINARY; PRT; 62 AA.  
 ID AAS90616;  
 AC AAS90616;  
 DT 27-APR-2004 (TrEMBLrel. 27, Created)  
 DT 27-APR-2004 (TrEMBLrel. 27, Last sequence update)  
 DT 27-APR-2004 (TrEMBLrel. 27, Last annotation update)  
 DE Putative glucosamine-fructose-6-phosphate aminotransferase  
 DE (Fragment).  
 OS uncultured soil bacterium.  
 OC Bacteria; environmental samples.  
 OX NCBI\_TaxID=164851;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RA Riesenfeld C.S., Goodman R.M., Handelsman J.;  
 RT "Uncultured soil bacteria are a reservoir of new antibiotic resistance  
 genes."  
 RL Submitted (MAR-2004) to the EMBL/GenBank/DBJ databases.

Query Match 81.2%; Score 39; DB 2; Length 1044;  
 Best Local Similarity 66.7%; Pred. No. 3.2e+02;  
 Matches 6; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

DR EMBL; AY566824; AAS90616.1; -;  
 KW Amino transferase; Transferase.  
 FT NON\_TER 1  
 SQ SEQUENCE 62 AA; 6835 MW; 4BFCBC9E94F35A4E CRC64;  
 Query Match 81.2%; Score 39; DB 2; Length 62;  
 Best Local Similarity 66.7%; Pred. No. 22;  
 Matches 6; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 SPVNLPPPEL 9  
 ||:|||||  
 DB 13 SPIQLPPEI 21

## RESULT 11

Q82X60 PRELIMINARY; PRT; 292 AA.  
 ID Q82X60;  
 AC Q82X60;  
 DT 01-JUN-2003 (TrEMBLrel. 24, Created)  
 DT 01-JUN-2003 (TrEMBLrel. 24, Last sequence update)  
 DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)  
 DE Possible pseudouridylylate synthase family 1.  
 GN OrderedLocusNames=NE0435;  
 OS Nitrosomonas europaea.  
 OC Bacteria; Proteobacteria; Betaproteobacteria; Nitrosomonadales;  
 OX Nitrosomonadaceae; Nitrosomonas.  
 OX NCBI\_TaxID=915;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=ATCC 19718 / IFO 14298;  
 RX MEDLINE=22586410; PubMed=12700255;  
 RA Chain P., Lamerdin J.E., Larimer F.W., Regala M., Lao V., Land M.L.,  
 RA Hauser L., Hooper A.B., Klotz M.G., Norton J., Sayavedra-Soto L.A.,  
 RA Arciero D.M., Holmes N.G., Whittaker M.M., Arp D.J.;  
 RT "Complete genome sequence of the ammonia-oxidizing bacterium and  
 RT obligate chemolithoautotroph Nitrosomonas europaea.";  
 RL J. Bacteriol. 185:2759-2773(2003).  
 CC -1- CATALYTIC ACTIVITY: Uracil + D-ribose 5-phosphate = pseudouridine  
 CC 5'-phosphate + H(2)O.  
 CC -1- SIMILARITY: Belongs to the pseudouridine synthase rsuA family.  
 DR EMBL; BX321857; CAD84346.1; -;  
 DR GO; GO:0009982; F:pseudouridylylate synthase activity; IEA.  
 DR GO; GO:0004730; F:pseudouridylylate synthase activity; IEA.  
 DR GO; GO:0003723; F:RNA binding; IEA.  
 DR GO; GO:0006396; P:RNA processing; IEA.  
 DR InterPro; IPR006145; Pseudou synth.  
 DR InterPro; IPR000748; Psi\_synth\_RSU.  
 DR InterPro; IPR002942; S4.  
 DR Pfam; PF01479; S4; 1.  
 DR ProDom; PD001819; Pseudou synth; 1.  
 DR SMART; SM00363; S4; 1.  
 DR TIGRfam; TIGR00093; Psi\_synth\_RSU; 1.  
 DR PROSITE; PS01149; PSI\_RSU; 1.  
 DR PROSITE; PS00889; S4; 1.  
 KW Complete proteome; Lyase.  
 SQ SEQUENCE 292 AA; 32704 MW; BE44A0D849219DBC CRC64;

Query Match 81.2%; Score 39; DB 2; Length 292;  
 Best Local Similarity 87.5%; Pred. No. 1.2e+02;  
 Matches 7; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2 PVNLPPPEL 9  
 ||:|||||  
 DB 245 PVNLPPPEL 252

## RESULT 12

Q89QS3 PRELIMINARY; PRT; 330 AA.  
 ID Q89QS3;  
 AC Q89QS3;  
 DT 01-JUN-2003 (TrEMBLrel. 24, Created)  
 DT 01-JUN-2003 (TrEMBLrel. 24, Last sequence update)

```

DT 01-MAR-2004 (TRENBLrel. 26, Last annotation update)
DE B113051 protein.
GN OrderedLocusNames=b113051;
OS Bradyrhizobium japonicum.
OC Bacteria; Proteobacteria; Alphaproteobacteria; Rhizobiales;
OC Bradyrhizobiaceae; Bradyrhizobium.
OX NCBI_TaxID=375;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=USDA110;
RX MEDLINE=2248498; PubMed=12597275;
RA Kaneko T., Nakamura Y., Sato S., Minamisawa K., Uchiyama T.,
RA Sasamoto S., Watanabe A., Idegawa K., Iriyuchi M., Kawashima K.,
RA Kohara M., Matsumoto M., Shimpo S., Tsuruoka H., Wada T., Yamada M.,
RA Tabata S.;
RT "Complete genomic sequence of nitrogen-fixing symbiotic bacterium
RT Bradyrhizobium japonicum USDA110."
RL DNA Res. 9:189-197(2002).
DR EMBL; AP005946; BAC48316.1; -.
DR GO; GO:0030288; C:periplasmic space (sensu Gram-negative Bact. . . ; IEA.
DR InterPro; IPR006311; Tat.
DR InterPro; IPR005064; UPF0065.
DR Pfam; PF03401; Bug; 1.
DR TIGRFAMs; TIGR01409; Tat_signal_seq; 1.
KW Complete proteome.
SQ SEQUENCE 330 AA; 34040 MW; 842B6CE06F95D932 CRC64;

Query Match 81.2%; Score 39; DB 2; Length 330;
Best Local Similarity 77.8%; Pred. No. 1.4e+02;
Matches 7; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 SPVNLPEL 9
Db 263 APKNLPEL 271

RESULT 13
Q9FVG6 PRELIMINARY; PRT; 854 AA.
AC Q9FVG6;
DT 01-MAR-2001 (TRENBLrel. 16, Created)
DT 01-MAR-2001 (TRENBLrel. 16, Last sequence update)
DT 01-JUN-2002 (TRENBLrel. 21, Last annotation update)
DE Transposase.
OS Zea mays (Maize).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
OC PACCAD clade; Panicoideae; Andropogoneae; Zea.
OX NCBI_TaxID=4577;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=W22; TRANSPOS=Donp14;
RX MEDLINE=21471138; PubMed=11587506;
RA Bercury S.D., Panavas T., Irenze K., Walker E.L.;
RT "Molecular analysis of the Dopia transposable element of maize."
RL Plant Mol. Biol. 47:341-351(2001).
DR EMBL; AF187822; AAG17043.1; -.
DR InterPro; IPR004242; Transposase_21.
DR Pfam; PF02992; Transposase_21; 1.
SQ SEQUENCE 854 AA; 99056 MW; C3F745C5EEB706EA CRC64;

Query Match 81.2%; Score 39; DB 2; Length 854;
Best Local Similarity 87.5%; Pred. No. 3.9e+02;
Matches 7; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2 PVNLPEL 9
Db 355 PVNLPEL 362

RESULT 14
SNFS_YEAST STANDARD; PRT; 905 AA.
ID -SNFS_YEAST

```

---

```

AC DT 01-NOV-1990 (Rel. 16, Created)
DT 01-OCT-1994 (Rel. 30, Last sequence update)
DT 05-JUN-2004 (Rel. 44, Last annotation update)
DE Transcription regulatory protein SNF5 (SWI/SNF complex component SNF5)
DE (Transcription factor TVE4).
DE Name=SNF5; Synonyms=TVE4, SWI10; OrderedLocusNames=YBR289W;
GN ORFNames=YBR2036;
GN Saccharomyces cerevisiae (Baker's yeast).
OS Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
OC Saccharomycetales; Saccharomycetaceae; Saccharomyces.
OX NCBI_TaxID=4932;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=MCY;
RX MEDLINE=91042489; PubMed=22333708;
RA Laurent B.C., Treitel M.A., Carlson M.;
RT "The SNF5 protein of Saccharomyces cerevisiae is a glutamine- and
RT proline-rich transcriptional activator that affects expression of a
RT broad spectrum of genes."
RL Mol. Cell. Biol. 10:5616-5625(1990).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=S288C;
RX MEDLINE=94378722; PubMed=8091861;
RA Holmstroem K., Brandt T., Kallioe T.;
RT "The sequence of a 32,420 bp segment located on the right arm of
RT chromosome II from Saccharomyces cerevisiae."
RL Yeast 10:S47-S62(1994).
CC -1- FUNCTION: Involved in transcriptional activation. The SWI/SNF
CC complex is required for the induced expression of a large number
CC of genes. This complex alters chromatin structure to facilitate
CC binding of gene-specific dedicated transcription factors.
CC -1- SUBUNIT: Component of the SWI/SNF global transcription activator
CC complex.
CC -1- SUBCELLULAR LOCATION: Nuclear.
CC -1- SIMILARITY: Belongs to the SNF5 family.
CC
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL Outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC or send an email to license@isb-sib.ch).
CC
CC EMBL; M36482; AAA35062.1; -.
CC EMBL; X76053; CAA53652.1; -.
CC EMBL; Z36158; CAA85254.1; -.
CC PIR; S44551; RGBY35.
CC IntAct; P18480; -.
CC Germline; 138832; -.
CC SGD; S0000493; SNF5.
CC InterPro; IPR006939; SNF5.
CC Pfam; PF04855; SNF5; 1.
CC Activator; Nuclear protein; Transcription regulation.
FT DOMAIN 31 270 Gln-rich.
FT DOMAIN 72 132 Pro-rich.
FT DOMAIN 272 324 Pro-rich.
FT DOMAIN 489 588 Asp/Glu-rich (acidic).
FT DOMAIN 714 882 Pro-rich.
FT DOMAIN 755 798 Arg/Lys-rich (basic).
FT CONFLICT 564 564 E -> D (in Ref. 1).
SQ SEQUENCE 905 AA; 102557 MW; A287B4A648DDIA35 CRC64;

Query Match 81.2%; Score 39; DB 1; Length 905;
Best Local Similarity 55.6%; Pred. No. 4.1e+02;
Matches 5; Conservative 4; Mismatches 0; Indels 0; Gaps 0;

QY 1 SPVNLPEL 9
Db 120 APINLPPQI 128

```



```
RESULT 15
Q9CM76
ID Q9CM76 PRELIMINARY; PRT; 1124 AA.
AC Q9CM76;
DT 01-JUN-2001 (TrEMBLrel. 17, Created)
DT 01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE RecC.
GN Name=recC; OrderedLocusNames=PM0961;
OS Pasteurella multocida.
OC Bacteria; Proteobacteria; Gammaproteobacteria; Pasteurellales;
OC Pasteurellaceae; Pasteurella.
OX NCBI_TaxID=747;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=Pm70;
RX MEDLINE=21145866; PubMed=11248100;
RA May B.J., Zhang Q., Li L.L., Paustian M.L., Whittam T.S., Kapur V.;
RT "Complete genomic sequence of Pasteurella multocida Pm70."
RL Proc. Natl. Acad. Sci. U.S.A. 98:3460-3465(2001).
DR EMBL; AE006135; AAK03045.1; --
DR GO; GO:0009338; C:exodeoxyribonuclease V complex; IEA.
DR GO; GO:0008854; F:exodeoxyribonuclease V activity; IEA.
DR InterPro; IPR006697; RecC.
DR Pfam; PF04257; Exonuc V.gamma; 1.
DR TIGRFAMS; TIGR01450; recC; 1.
KW Complete proteome.
SQ SEQUENCE 1124 AA; 130520 MW; F249057CEPAC9C84 CRC64;

Query Match 81.2%; Score 39; DB 2; Length 1124;
Best Local Similarity 87.5%; Pred. No. 5.2e+02;
Matches 7; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2 PVNLPPEL 9
Db 223 PVNLPPEL 230

Search completed: November 19, 2004, 23:44:27
Job time : 38.1972 secs
```

This Page Blank (uspto,

GenCore version 5.1.6  
Copyright (c) 1993 - 2004 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: November 19, 2004, 23:28:53 ; Search time 110.028 Seconds  
(without alignments)  
202.141 Million cell updates/sec

Title: US-10-068-725-4\_COPY\_105\_166

Perfect score: 315  
Sequence: 1 ENKLSPVNLPELRRQSG.....SPALPLKLUSADQVALVYST 62

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 2002273 seqs, 358729299 residues

Total number of hits satisfying chosen parameters: 2002273

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : A\_Geneseq\_23Sep04:\*  
1: Geneseqp1980s:\*  
2: Geneseqp1990s:\*  
3: Geneseqp2000s:\*  
4: Geneseqp2001s:\*  
5: Geneseqp2002s:\*  
6: Geneseqp2003as:\*  
7: Geneseqp2003bs:\*  
8: Geneseqp2004s:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Score | Query Match | Length | DB ID | Description        |
|------------|-------|-------------|--------|-------|--------------------|
| 1          | 315   | 100.0       | 166    | 2     | Aaw75785 Human lym |
| 2          | 315   | 100.0       | 166    | 5     | Aae15494 Human TAC |
| 3          | 315   | 100.0       | 246    | 6     | Abp97720 Amino aci |
| 4          | 315   | 100.0       | 246    | 8     | Adk00762 Native hu |
| 5          | 315   | 100.0       | 247    | 3     | Aay93998 Human BR4 |
| 6          | 315   | 100.0       | 247    | 7     | Abp61797 Human RYZ |
| 7          | 315   | 100.0       | 265    | 4     | Aae09244 Human TAC |
| 8          | 315   | 100.0       | 266    | 6     | Abp97723 Amino aci |
| 9          | 315   | 100.0       | 293    | 2     | Aaw75783 Human lym |
| 10         | 315   | 100.0       | 293    | 3     | Aab36312 Human neu |
| 11         | 315   | 100.0       | 293    | 3     | Aay94000 A transme |
| 12         | 315   | 100.0       | 293    | 4     | Aae09240 Human TAC |
| 13         | 315   | 100.0       | 293    | 4     | Aay71914 Human tum |
| 14         | 315   | 100.0       | 293    | 5     | Aao14130 Human tra |
| 15         | 315   | 100.0       | 293    | 5     | Abb81488 Human TAC |
| 16         | 315   | 100.0       | 293    | 5     | Aau99512 Human TAC |
| 17         | 315   | 100.0       | 293    | 5     | Aae28962 Human TAC |
| 18         | 315   | 100.0       | 293    | 5     | Aau75408 Tumour ne |
| 19         | 315   | 100.0       | 293    | 5     | Aau09900 Human AGP |
| 20         | 315   | 100.0       | 293    | 5     | Aae15493 Human tra |
| 21         | 315   | 100.0       | 293    | 5     | Abg71496 Human tum |
| 22         | 315   | 100.0       | 293    | 6     | Aae35211 Human TAC |
| 23         | 315   | 100.0       | 293    | 6     | Abp60551 Human tum |
| 24         | 315   | 100.0       | 293    | 6     | Abp97716 Amino aci |
| 25         | 315   | 100.0       | 293    | 6     | Aao29592 Human DIT |

|    |       |       |     |   |                    |
|----|-------|-------|-----|---|--------------------|
| 26 | 315   | 100.0 | 293 | 7 | ADF72628 Human tum |
| 27 | 315   | 100.0 | 293 | 7 | Adf77379 Human tum |
| 28 | 315   | 100.0 | 293 | 8 | Adk00754 Native hu |
| 29 | 315   | 100.0 | 293 | 8 | Adj92514 Human TAC |
| 30 | 315   | 100.0 | 293 | 8 | Adn03174 Human TAC |
| 31 | 315   | 100.0 | 294 | 8 | Adk00765 hTACI epl |
| 32 | 315   | 100.0 | 312 | 5 | Aao14135 Protein o |
| 33 | 310   | 98.4  | 397 | 5 | Aae15498 Human TAC |
| 34 | 300.5 | 95.4  | 291 | 5 | Aau10949 Human AGP |
| 35 | 287   | 91.1  | 404 | 5 | Aao14136 Protein o |
| 36 | 279.5 | 88.7  | 57  | 5 | Aau10953 Human AGP |
| 37 | 260   | 82.5  | 392 | 6 | Aae35223 Human TAC |
| 38 | 141.5 | 44.9  | 249 | 3 | Aay94006 A murine  |
| 39 | 85    | 27.0  | 357 | 6 | Aae35226 Human TAC |
| 40 | 84.5  | 26.8  | 702 | 4 | Abb63821 Drosophil |
| 41 | 66    | 21.0  | 428 | 7 | Abp75685 Pseudomon |
| 42 | 66    | 21.0  | 505 | 2 | Aaw61027 Murine gu |
| 43 | 66    | 21.0  | 535 | 2 | Aaw61028 Murine gu |
| 44 | 66    | 21.0  | 554 | 2 | Aaw61026 Murine gu |
| 45 | 64    | 20.3  | 88  | 3 | Aag33433 Zea mays  |

ALIGNMENTS

RESULT 1  
AAW75785  
ID AAW75785 standard; protein; 166 AA.  
XX  
AC AAW75785;  
XX  
DT 18-JAN-1999 (first entry)  
XX  
DE Human lymphocyte surface receptor extracellular domain.  
XX  
KW TACI; transmembrane activator and CAML-interactor;  
KW calcium signal-modulating cyclophilin ligand; human;  
KW lymphocyte surface receptor; human; B-cell; B lymphocyte; infection;  
KW cancer; rheumatoid arthritis; autoimmune disease; glomerulonephritis;  
KW immunosuppressive; graft versus host disease; transplant rejection;  
KW therapy; signal transduction.  
XX  
OS Homo sapiens.  
XX  
PN WO9839361-A1.  
XX  
PD 11-SEP-1998.  
XX  
PF 03-MAR-1998; 98WO-US004270.  
PR 03-MAR-1997; 97US-00810572.  
PA (SJUD-) ST JUDE CHILDREN'S RES HOSPITAL.  
PI Bram RJ, Von Bulow G;  
DR WPI: 1998-506346/43.  
XX N-PSDB; AAV57330.  
XX  
PT New isolated transmembrane activator protein - used to develop products  
PT for treating e.g. infections, cancers, autoimmune and inflammatory  
XX conditions, transplant rejection or graft-versus-host disease.  
PS Claim 8; Page 73; 89pp; English.  
CC This is the amino acid sequence of the N-terminal, i.e. the  
CC extracellular, domain of novel human transmembrane activator and CAML-  
CC interactor (TACI) protein (see AAW75783). TACI is a lymphocyte receptor  
CC protein that is involved in the calcium activation pathway. It is  
CC normally present in B-lymphocytes, and to a much lesser extent in  
CC immature T-lymphocytes, and can therefore be targeted to specifically  
CC regulate B cell responses without affecting T cell activity. The  
CC extracellular domain of TACI functions as a binding site for a ligand

that stimulates the activation of the cell by inducing the binding of the C-terminal portion (see AAW75784) of TACI to the N-terminal domain of CAML. A recombinant form of the extracellular portion of TACI acts as a dominant-negative or blocking agent and acts to suppress the immune system. It can be used to treat or prevent autoimmune disease, graft rejection or graft versus host disease. The extracellular region is also used in a claimed method for identifying a ligand for TACI, in which binding of a candidate molecule is determined by detecting cellular activation of the AP-1, CAMP or NF- $\kappa$ B pathway, of NF-AT transcription factor, or of NF-AT dependent transcription

XX SQ Sequence 166 AA;

Query Match 100.0%; Score 315; DB 2; Length 166;  
Best Local Similarity 100.0%; Pred. No. 4.8e-33;  
Matches 62; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 ENKLRSPVNLPELRRQRSGEVENNSDNGRYQGLEHRSSEASPALPGLKLSADQVALVY 60  
DB 105 ENKLRSPVNLPELRRQRSGEVENNSDNGRYQGLEHRSSEASPALPGLKLSADQVALVY 164  
QY 61 ST 62  
DB 165 ST 166

# RESULT 2

AAE15494  
ID AAE15494 standard; protein; 166 AA.

AC AAE15494;

DT 12-MAR-2002 (first entry)

DE Human TACI extracellular domain.

XX Human; transmembrane activator and intracellular CAML interactor; TACI;  
XX cytosolic; B cell maturation protein; BCMA; tumour necrosis factor; TNF;  
KW lymphoproliferative disorder; tumour; lung; gastrointestinal; pancreatic;  
KW prostate; inflammation; immune disorder; diarrhoea; psoriasis; colitis;  
KW drug allergy; dermatitis; pneumonia; asthma; inflammatory bowel disease;  
KW Crohn's disease; scleroderma; autoimmune disease; multiple sclerosis;  
KW human immunodeficiency virus; HIV; systemic lupus erythematosus; cancer;  
KW rheumatoid arthritis; atherosclerosis.

XX Homo sapiens.

XX WO200187979-A2.

XX 22-NOV-2001.

XX 14-MAY-2001; 2001WO-US015567.

XX 12-MAY-2000; 2000US-0204039P.

XX 27-JUN-2000; 2000US-0214591P.

XX 14-MAY-2001; 2001US-00214591.

XX (AMGE-) AMGEN INC.

XX Theill LE, Yu G;

XX WPI; 2002-066686/09.

XX Inhibiting activity of B cell maturation protein and/or transmembrane  
XX activator and intracellular cyclophilin ligand interactor, by  
XX administering a binding partner for APRIL, a tumor necrosis factor family  
XX ligand.

XX Claim 1; Fig 12A; 94pp; English.

XX The invention relates to a method for inhibiting TACI (transmembrane  
XX activator and intracellular CAML interactor) and/or B cell maturation  
XX protein (BCMA) activity in a mammal. The method comprises administering a

CC specific binding partner for APRIL (G70, a tumour necrosis factor-TNF  
CC family ligand), having the consensus region of TACI, BCMA, or the TACI/  
CC BCMA extracellular consensus sequence, but not the extracellular region  
CC of TACI or BCMA. The method is useful for inhibiting activity of TACI  
CC and/or BCMA in a mammal which is useful for treating B-cell or T-cell  
CC lymphoproliferative disorders, one or more solid tumours such as lung,  
CC gastrointestinal, pancreatic or prostate tumour. APRIL, BCMA and TACI  
CC antagonists are useful for treating inflammation and immune function  
CC diseases such as diarrhoea, psoriasis, allergies, pneumonia, atopic  
CC dermatitis, respiratory allergic disease (asthma, hypersensitivity lung  
CC disease), drug and insect sting allergy, inflammatory bowel disease  
CC (Crohn's disease, colitis), scleroderma, autoimmune disease (multiple  
CC sclerosis, rheumatoid arthritis, systemic lupus erythematosus), fungal,  
CC bacterial, protozoal and viral infections (HIV), atherosclerosis, cancer  
CC with leucocyte infiltration of the skin or organs. The present sequence  
CC is human TACI protein extracellular domain

XX SQ Sequence 166 AA;

Query Match 100.0%; Score 315; DB 5; Length 166;  
Best Local Similarity 100.0%; Pred. No. 4.8e-33;  
Matches 62; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ENKLRSPVNLPELRRQRSGEVENNSDNGRYQGLEHRSSEASPALPGLKLSADQVALVY 60  
DB 105 ENKLRSPVNLPELRRQRSGEVENNSDNGRYQGLEHRSSEASPALPGLKLSADQVALVY 164  
QY 61 ST 62  
DB 165 ST 166

# RESULT 3

ABP97720  
ID ABP97720 standard; protein; 246 AA.

XX AC ABP97720;

XX 28-MAY-2003 (first entry)

XX Amino acid sequence of human TACI receptor.

XX Human; TACI; BR3; receptor; tumour necrosis factor ligand; TNF ligand;  
XX TALL-1; April; systemic lupus erythematosus.

XX Homo sapiens.

XX WO2003014294-A2.

XX 20-FEB-2003.

XX 24-JUL-2002; 2002WO-US023487.

XX 03-AUG-2001; 2001US-0310114P.

XX 30-APR-2002; 2002US-0377171P.

XX (GETH ) GENENTECH INC.

XX Dixit V, Grewal I, Ridgway J, Yan M;

XX WPI; 2003-256560/25.

XX N-PSDB; AB268874.

XX New nucleic acid encoding a TACIs or BR3 polypeptide, useful for  
XX preparing a composition for treating systemic lupus erythematosus.

XX Disclosure; Fig 5B; 153pp; English.

XX The present sequence represents a human TACI polypeptide. The  
XX specification also describes BR3 polypeptides. TACI and BR3 are  
XX receptors. Tumour necrosis factor (TNF) family ligands TALL-1 and April  
XX bind to the TACI receptor, while TNF family ligands TALL-1 also binds to  
XX BR3 receptor. The TACI and BR3 receptor nucleic acid is useful for

CC preparing a composition for treating systemic lupus erythematosus

XX Sequence 246 AA;  
 Query Match 100.0%; Score 315; DB 6; Length 246;  
 Best Local Similarity 100.0%; Pred. No. 8.1e-33;  
 Matches 62; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 ENKLSPVNLPELRQRSGEVENNSDGRYQGLEHGRGSEASPALPGLKLSADQVALVY 60  
 DB 59 ENKLSPVNLPELRQRSGEVENNSDGRYQGLEHGRGSEASPALPGLKLSADQVALVY 118  
 QY 61 ST 62  
 DB 119 ST 120

## RESULT 4

ADK00762  
 ID ADK00762 standard; protein; 246 AA.

XX AC  
 ADK00762;

DT 06-MAY-2004 (first entry)

DE Native human TACIs.

XX CAML interactor receptor; TACI; Cytostatic; Antiinflammatory;

KW Dermatological; Immunosuppressive; Antirheumatic; Antiarthritic;

KW Antidiabetic; Neuroprotective; Antiasthmatic; Antiallergic; Anti-HIV;

KW Antibacterial; antiparasitic; systemic lupus erythematosus;

KW diabetes mellitus; AIDS.

XX Homo sapiens.

OS  
 WO2004011611-A2.

XX PD 05-FEB-2004.

XX PF 25-JUL-2003; 2003WO-US023421.

XX PR 25-JUL-2002; 2002US-0398530P.

XX PA (GETH ) GENENTECH INC.

XX PI Chuntharapai A, Grewal I, Kim KJ, Yan M;

XX WPI; 2004-143841/14.

DR N-PSDB; ADK00761.

XX New anti-TACI receptor monoclonal antibody, useful for diagnosing and  
 PT treating pathological conditions associated with tumor necrosis factor,  
 PT e.g. cancer or immune-related disease, such as rheumatoid arthritis or  
 PT psoriasis.

XX PS Disclosure; SEQ ID NO 14; 110pp; English.

XX The present invention relates to an isolated monoclonal antibody which  
 CC binds to a transmembrane activator of and CAML interactor (TACI)  
 CC receptor. The TACI antibodies are useful for modulating TALL-1 or TACI  
 CC polypeptide biological activity in mammalian cells, or for diagnosing and  
 CC treating pathological conditions associated with TNF and TNF receptor-  
 CC related molecules, e.g. cancer or immune-related disease, such as  
 CC systemic lupus erythematosus, rheumatoid arthritis, Sjogren's syndrome,  
 CC systemic vasculitis, diabetes mellitus, Crohn's disease,  
 CC glomerulonephritis, multiple sclerosis, psoriasis, asthma, urticaria or  
 CC infectious diseases including AIDS, hepatitis infection, bacterial  
 CC infection, fungal infection, protozoal infection and parasitic infection.  
 CC The present sequence represents native human TACIs.

XX Sequence 246 AA;

XX Query Match 100.0%; Score 315; DB 8; Length 246;

Best Local Similarity 100.0%; Pred. No. 8.1e-33;  
 Matches 62; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ENKLSPVNLPELRQRSGEVENNSDGRYQGLEHGRGSEASPALPGLKLSADQVALVY 60  
 DB 59 ENKLSPVNLPELRQRSGEVENNSDGRYQGLEHGRGSEASPALPGLKLSADQVALVY 118

QY 61 ST 62

DB 119 ST 120

## RESULT 5

AAY93998

ID AAY93998 standard; protein; 247 AA.

XX AC AAY93998;

DT 20-OCT-2000 (first entry)

DE Human BR43x2, an isoform of the TACI receptor.

XX Human; BR43x2; TACI receptor; extracellular domain; BCMA; B cell protein;  
 KW transmembrane activator and CAML-interactor; tumour necrosis factor; TNF;  
 KW ztnf4 activity; antibody production; autoimmune disease; amyloidosis;  
 KW systemic lupus erythematosus; myasthenia gravis; multiple sclerosis;  
 KW rheumatoid arthritis; asthma; bronchitis; emphysema; pyelonephritis;  
 KW end stage renal failure; glomerulonephritis; vasculitis; nephritis;  
 KW renal neoplasia; multiple myeloma; lymphoma; light chain neuropathy;  
 KW immune response; immunosuppression; graft rejection; joint pain;  
 KW graft versus host disease; inflammation; swelling; anaemia; septic shock;  
 KW insulin dependent diabetes mellitus; Crohn's disease; hypertension;  
 KW renal artery stenosis; occlusion; cholesterol; renal emboli.

XX OS Homo sapiens.

XX FH Key Location/Qualifiers

FT Domain 1..120

FT /note= "extracellular domain"

FT Region 25..58

FT /note= "cysteine-rich pseudo repeat"

FT Domain 121..133

FT /note= "transmembrane domain"

FT Domain 134..247

FT /note= "cytoplasmic domain"

XX WO200040716-A2.

XX PD 13-JUL-2000.

XX PF 07-JAN-2000; 2000WO-US000396.

XX PR 07-JAN-1999; 99US-00226533.

XX PA (ZYMO ) ZYMOGENETICS INC.

XX PI Gross JA, Xu W, Madden K, Yee DP;

XX WPI; 2000-452538/39.

DR N-PSDB; AAA58556.

XX Inhibiting ztnf4 activity in a mammal, to treat autoimmune diseases,  
 PT renal disease, graft versus host disease, and inflammation, comprises  
 PT administering a BR43x2, TACI or BCMA extracellular domain polypeptide.

XX Claim 62; Page 145; 175pp; English.

XX The present sequence represents a human BR43x2 polypeptide, which is an  
 CC isoform of the transmembrane activator and CAML-interactor (TACI)  
 CC receptor. TACI is a tumour necrosis factor (TNF) receptor. The  
 CC extracellular domains of BR43x2, TACI or BCMA (a related B cell protein)  
 CC contain a cysteine rich domain, and are used for inhibiting ztnf4  
 CC activity. Ztnf4 is a TNF ligand. They may also be used for inhibiting

CC BR43x2, TAC1 or BCMA receptor-ligand engagement associated with activated  
 CC or resting B lymphocytes, effector T-cells, or with antibody production.  
 CC The antibody production is associated with an autoimmune disease selected  
 CC from systemic lupus erythematosus, myasthenia gravis, multiple sclerosis  
 CC and rheumatoid arthritis. The ztnf4 activity and BR43x2, TAC1 or BCMA  
 CC receptor-ligand engagement is associated with asthma, bronchitis,  
 CC emphysema, end stage renal failure, glomerulonephritis, vasculitis,  
 CC nephritis, pyelonephritis, renal neoplasms, multiple myelomas, lymphomas,  
 CC light chain neuropathy, amyloidosis, moderating immune response,  
 CC immunosuppression, graft rejection, graft versus host disease,  
 CC inflammation, insulin dependent diabetes mellitus, Crohn's disease, joint  
 CC pain, swelling, anaemia, or septic shock. BR43x2, TAC1, and BCMA  
 CC polypeptides, fusions, antibodies, agonists or antagonists can be used to  
 CC treat hypertension, renal artery stenosis, or occlusion, and cholesterol  
 CC or renal emboli

XX Sequence 247 AA;

Query Match 100.0%; Score 315; DB 3; Length 247;  
 Best Local Similarity 100.0%; Pred. No. 8.1e-33;  
 Matches 62; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ENKLRSPVNLPPELRRQSGVEVNSDNGRYQGLEHGRGSEASPALPGLKLSADQVALVY 60  
 |||||  
 Db 59 ENKLRSPVNLPPELRRQSGVEVNSDNGRYQGLEHGRGSEASPALPGLKLSADQVALVY 118  
 |||||  
 Qy 61 ST 62  
 ||  
 Db 119 ST 120

RESULT 6

ABR61797  
 ID ABR61797 standard; protein; 247 AA.

XX ABR61797;

DT 12-SEP-2003 (first entry)

DE Human RYZN polypeptide.

XX RYZN; TNFRSF; tumour necrosis factor receptor; antiarteriosclerotic;  
 KW type III transmembrane protein; antidiabetic; hypotensive; antilipemic;  
 KW human.

XX Homo sapiens.

XX Key Location/Qualifiers

FT Domain 1..113  
 /note= "extracellular domain"  
 FT Domain 114..136  
 /note= "transmembrane domain"  
 FT Domain 137..247  
 /note= "intracellular domain"

XX WO2003045421-A1.

XX 05-JUN-2003.

XX 03-OCT-2002; 2002WO-IB004581.

XX 28-NOV-2001; 2001US-0334152P.

XX (GEST ) GENSET SA.

XX Dyalynas D, Scalia A, Lucas J, Briggs K;

XX WPI; 2003-513616/48.

XX N-PSDB; ACC84638.

XX New agonists or antagonists of RYZN activity, useful for increasing or  
 PT reducing body weight, for maintaining weight loss, and for preventing or  
 PT treating an obesity-related disease or disorder, e.g. atherosclerosis or

PT diabetes.

XX Example; Page 32-33; 37pp; English.

XX The invention relates to an agonist or antagonist of RYZN activity. RYZN  
 CC is a member of the Tumour Necrosis Factor Receptor Super family (TNFRSF)  
 CC and is a Type III transmembrane protein. The agonist or antagonist of  
 CC RYZN activity, or compositions comprising them is useful for preventing  
 CC or treating an obesity-related disease or disorder, such as insulin  
 CC resistance, hyperlipidemia, atherosclerosis, diabetes, hypertension,  
 CC syndrome X, and hyperuricemia. These may also be used to increase or  
 CC reduce body weight, or maintain weight loss. The present sequence  
 CC represents the human RYZN polypeptide

XX Sequence 247 AA;

Query Match 100.0%; Score 315; DB 7; Length 247;  
 Best Local Similarity 100.0%; Pred. No. 8.1e-33;  
 Matches 62; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ENKLRSPVNLPPELRRQSGVEVNSDNGRYQGLEHGRGSEASPALPGLKLSADQVALVY 60  
 |||||  
 Db 59 ENKLRSPVNLPPELRRQSGVEVNSDNGRYQGLEHGRGSEASPALPGLKLSADQVALVY 118  
 |||||  
 Qy 61 ST 62  
 ||  
 Db 119 ST 120

RESULT 7

AAE09244

ID AAE09244 standard; protein; 265 AA.

XX AAE09244;

XX 19-NOV-2001 (first entry)

DE Human TAC1 splice variant protein.

XX Human; TNF; tumour necrosis factor; TALL-1; APRIL; TNF receptor; TNFR;  
 KW TAC1; BCMA; therapy; cancer; leukaemia; myeloma; lymphoma;  
 KW autoimmune disease; rheumatoid arthritis; multiple sclerosis; psoriasis.

XX Homo sapiens.

XX WO200160397-A1.

XX 23-AUG-2001.

XX 28-NOV-2000; 2000WO-US032378.

XX 16-FEB-2000; 2000US-0182938P.

XX 22-AUG-2000; 2000US-0226986P.

XX (GETH ) GENENTECH INC.

XX Ashkenazi AJ, Dodge KH, Grewal I, Kim KJ, Marsters SA, Pitti RM;  
 PI Yan M;

XX WPI; 2001-541628/60.

XX Inhibiting or neutralizing TALL-1 or APRIL polypeptide biological  
 PT activity, for treating autoimmune disorders and cancer, comprises  
 PT exposing the cells to TALL-1 or APRIL polypeptide agonists or  
 PT antagonists.

XX Example 1; Fig 6; 160pp; English.

XX The invention relates to methods of using one or more agonists or  
 CC antagonists to modulate the activity of the members of TNF (tumour  
 CC necrosis factor) especially TALL-1, APRIL and TNF receptor (TNFR) e.g.  
 CC TAC1 or BCMA. The method is useful for treating pathological conditions  
 CC or diseases associated with increased TALL-1 and APRIL expression or

CC activity, TALL-1 and APRIL antagonists are used to block the interaction  
 CC between APRIL and TALL-1 with TACI or BCMA. They are useful for treating  
 CC a mammal suffering from cancer such as leukaemia, lymphoma, myeloma,  
 CC cancers of lung and colon and autoimmune diseases e.g. rheumatoid  
 CC arthritis, multiple sclerosis, psoriasis and lupus erythematosus. The  
 CC present sequence is human TACI splice variant protein  
 XX  
 XX SQ Sequence 265 AA;

Query Match 100.0%; Score 315; DB 4; Length 265;  
 Best Local Similarity 100.0%; Pred. No. 8.9e-33;  
 Matches 62; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ENKLSPVNLPELRRQRSGEVENNSDNGRYQGLEHGRGSEASPALPGLKLSADQVALVY 60  
 |||||  
 DB 105 ENKLSPVNLPELRRQRSGEVENNSDNGRYQGLEHGRGSEASPALPGLKLSADQVALVY 164  
 |||||

QY 61 ST 62

DB 165 ST 166

# RESULT 8

ID ABP97723 standard; protein; 266 AA.

AC ABP97723;

DT 28-MAY-2003 (first entry)

DE Amino acid sequence of an alternatively spliced human TACI receptor.

XX Human; TACI; BR3; receptor; tumour necrosis factor ligand; TNF ligand;  
 KW TALL-1; April; systemic lupus erythematosus.  
 XX Homo sapiens.

OS

XX WO2003014294-A2.

XX 20-FEB-2003.

XX 24-JUL-2002; 2002WO-US023487.

XX 03-AUG-2001; 2001US-0310114P.

XX 30-APR-2002; 2002US-0377171P.

XX (GETH ) GENENTECH INC.

XX Dixit V, Grewal I, Ridgway J, Yan M;

XX WPI; 2003-256560/25.

PT New nucleic acid encoding a TACIs or BR3 polypeptide, useful for  
 PT preparing a composition for treating systemic lupus erythematosus.

XX Disclosure; Fig 8; 153pp; English.

XX The present sequence represents an alternatively spliced human TACI  
 CC polypeptide. The specification also describes BR3 polypeptides. TACI and  
 CC BR3 are receptors. Tumour necrosis factor (TNF) family ligands TALL-1 and  
 CC April bind to the TACI receptor, while TNF family ligands TALL-1 also  
 CC binds to BR3 receptor. The TACI and BR3 receptor nucleic acid is useful  
 CC for preparing a composition for treating systemic lupus erythematosus  
 XX

XX SQ Sequence 266 AA;

Query Match 100.0%; Score 315; DB 6; Length 266;  
 Best Local Similarity 100.0%; Pred. No. 9e-33;  
 Matches 62; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ENKLSPVNLPELRRQRSGEVENNSDNGRYQGLEHGRGSEASPALPGLKLSADQVALVY 60  
 |||||  
 DB 105 ENKLSPVNLPELRRQRSGEVENNSDNGRYQGLEHGRGSEASPALPGLKLSADQVALVY 164  
 |||||

QY 61 ST 62

DB 165 ST 166

# RESULT 9

AAW75783

XX AAW75783 standard; protein; 293 AA.

AC AAW75783;

DT 18-JAN-1999 (first entry)

XX Human lymphocyte surface receptor TACI.

XX TACI; transmembrane activator and CAML-interactor;  
 KW calcium signal-modulating cyclophilin ligand; human;  
 KW lymphocyte surface receptor; human; B-cell; B lymphocyte; infection;  
 KW cancer; rheumatoid arthritis; autoimmune disease; glomerulonephritis;  
 KW immunosuppressive; graft versus host disease; transplant rejection;  
 KW therapy.

XX Homo sapiens.

XX Key

FT Domain

FT 1..166

FT /label= Extracellular\_domain

FT /note= "Claim 8"

FT Peptide

FT 34..71

FT /note= "TNFR\_NGFR motif"

FT Domain

FT 167..186

FT /label= Transmembrane\_domain

FT Domain

FT 187..294

FT /label= Cytoplasmic\_domain

FT /note= "Claim 6"

XX WO98393361-A1.

XX 11-SEP-1998.

XX 03-MAR-1998; 98WO-US004270.

XX 03-MAR-1997; 97US-00810572.

XX (SUJD-) ST JUDE CHILDREN'S RES HOSPITAL.

XX Bram RJ, Von Bulow G;

XX WPI; 1998-506346/43.

XX N-PSDB; AAV57328.

PT New isolated transmembrane activator protein - used to develop products  
 PT for treating e.g. infections, cancers, autoimmune and inflammatory  
 PT conditions, transplant rejection or graft-versus-host disease.

XX Claim 20; Fig 2a; 89pp; English.

XX This is the amino acid sequence of novel human transmembrane activator  
 CC and CAML-interactor (TACI) protein, a lymphocyte receptor protein that is  
 CC involved in the calcium activation pathway. TACI is normally present in B  
 CC -lymphocytes, and to a much lesser extent in immature T-lymphocytes, and  
 CC can therefore be targeted to specifically regulate B cell responses  
 CC without affecting T cell activity. TACI cDNA (seeV57328) was isolated  
 CC from a B-lymphocyte cDNA library using a yeast two-hybrid assay. Also  
 CC claimed are the C-terminal (see AAW75784) and N-terminal (see AAW75785)  
 CC fragments of TACI, recombinant DNA constructs, unicellular hosts, and  
 CC antibodies to TACI protein. Methods are claimed for identifying a ligand  
 CC for TACI and for identifying immunosuppressive drugs that selectively  
 CC block the action of B lymphocytes without affecting mature T lymphocytes.  
 CC TACI can be activated to increase immune system activity, e.g. for  
 CC treating infections or cancers. It can be blocked to provide  
 CC immunosuppression, e.g. for treating autoimmune and inflammatory

CC conditions such as immune complex- induced vasculitis.  
 CC glomerulonephritis, haemolytic anaemia, myasthenia gravis, type II  
 CC collagen-induced arthritis, experimental allergic and hyperacute  
 CC xenograft rejection, rheumatoid arthritis, systemic lupus erythematosus,  
 CC transplant rejection, cancer or graft versus host disease  
 XX

SQ Sequence 293 AA;  
 Query Match 100.0%; Score 315; DB 2; Length 293;  
 Best Local Similarity 100.0%; Pred. No. 1e-32;  
 Matches 62; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ENKLRSPVNLPPELRRQRSGEVNNSDNGRYQGLEHRGSEASPALPGLKLSADQVALVY 60  
 |||||  
 DB 105 ENKLRSPVNLPPELRRQRSGEVNNSDNGRYQGLEHRGSEASPALPGLKLSADQVALVY 164  
 |||||

QY 61 ST 62  
 ||  
 DB 165 ST 166

RESULT 10  
 AAB36312  
 ID AAB36312 standard; protein; 293 AA.  
 XX  
 AC AAB36312;  
 DT 26-FEB-2001 (first entry)  
 XX  
 DE Human neutrokin-alpha binding protein TR17 SEQ ID NO:2.  
 KW Human; neutrokin-alpha binding protein; NAR protein; TR17; cytostatic;  
 KW immunosuppressive; neutrotropic; neuroprotective; antiviral; anti-allergic;  
 KW hepatotropic; antidiabetic; anti-inflammatory; anti-ulcer; cardiant;  
 KW ophthalmological; gene therapy; immunodeficiency disorder; diagnosis;  
 KW autoimmune disorder.  
 XX  
 OS Homo sapiens.  
 XX  
 PN WO200058362-A1.  
 XX  
 PD 05-OCT-2000.  
 XX  
 PF 24-MAR-2000; 2000WO-US007966.  
 XX  
 PR 26-MAR-1999; 99US-0126599P.  
 XX  
 PR 10-MAR-2000; 2000US-0188208P.  
 XX  
 PA (HUMA-) HUMAN GENOME SCI INC.  
 XX  
 PI Ruben SM, Ullrich S, Baker K;  
 XX  
 DR WPI; 2000-602359/57.  
 DR N-PSDB; AAC64602.  
 XX  
 PT Nucleic acid encoding a neutrokin-alpha receptor (NAR) such as TR17,  
 PT useful for producing TR17 protein which is used in the treatment and  
 PT diagnosis of autoimmune and immunodeficiency disorders.  
 XX  
 PS Claim 1; Fig 1; 398pp; English.  
 XX  
 CC The present sequence represents the human neutrokin-alpha binding (NAR)  
 CC protein designated TR17. TR17 has cytostatic, immunosuppressive,  
 CC neutrotropic, neuroprotective, antiviral, anti-allergic, hepatotropic,  
 CC antidiabetic, anti-inflammatory, anti-ulcer, cardiant and ophthalmological  
 CC activities and can be used in gene therapy. The TR17 protein and  
 CC antibodies are useful for treating and diagnosing immunodeficiency  
 CC disorders and autoimmune disorders. The TR17 polypeptides,  
 CC polynucleotides, antibodies, agonists and/or antagonists are used for  
 CC treating various other diseases defined in the specification and as  
 CC research tools for studying the phenotypic effects that result from  
 CC inhibiting TR17/TR17 ligand interactions on various cell types  
 XX

SQ Sequence 293 AA;  
 Query Match 100.0%; Score 315; DB 3; Length 293;  
 Best Local Similarity 100.0%; Pred. No. 1e-32;  
 Matches 62; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ENKLRSPVNLPPELRRQRSGEVNNSDNGRYQGLEHRGSEASPALPGLKLSADQVALVY 60  
 |||||  
 DB 105 ENKLRSPVNLPPELRRQRSGEVNNSDNGRYQGLEHRGSEASPALPGLKLSADQVALVY 164  
 |||||

QY 61 ST 62  
 ||  
 DB 165 ST 166

RESULT 11  
 AAY94000  
 ID AAY94000 standard; protein; 293 AA.  
 XX  
 AC AAY94000;  
 XX  
 DT 20-OCT-2000 (first entry)  
 XX  
 DE A transmembrane activator and CAML-interactor (TACI).  
 XX  
 KW Human; BR43x2; TACI receptor; extracellular domain; BCMA; B cell protein;  
 KW transmembrane activator and CAML-interactor; tumour necrosis factor; TNF;  
 KW ztnf4 activity; antibody production; autoimmune disease; amyloidosis;  
 KW systemic lupus erythematosus; myasthenia gravis; multiple sclerosis;  
 KW rheumatoid arthritis; asthma; bronchitis; emphysema; pyelonephritis;  
 KW end stage renal failure; glomerulonephritis; vasculitis; nephritis;  
 KW renal neoplasm; multiple myeloma; lymphoma; light chain neuropathy;  
 KW immune response; immunosuppression; graft rejection; joint pain;  
 KW graft versus host disease; inflammation; swelling; anaemia; septic shock;  
 KW insulin dependent diabetes mellitus; Crohn's disease; hypertension;  
 KW renal artery stenosis; occlusion; cholesterol; renal emboli.  
 XX  
 OS Homo sapiens.  
 XX  
 PN WO200040716-A2.  
 XX  
 PD 13-JUL-2000.  
 XX  
 PF 07-JAN-2000; 2000WO-US000396.  
 XX  
 PR 07-JAN-1999; 99US-00226533.  
 XX  
 PA (ZYMO) ZYMOGENETICS INC.  
 XX  
 PI Gross JA, Xu W, Madden K, Yee DP;  
 XX  
 DR WPI; 2000-452538/39.  
 DR N-PSDB; AAA58558.  
 XX  
 PT Inhibiting ztnf4 activity in a mammal, to treat autoimmune diseases,  
 PT renal disease, graft versus host disease, and inflammation, comprises  
 PT administering a BR43x2, TACI or BCMA extracellular domain polypeptide.  
 XX  
 PS Disclosure; Page 149-150; 175pp; English.  
 XX  
 CC The present sequence represents a human transmembrane activator and CAML-  
 CC interactor (TACI) receptor. TACI is a tumour necrosis factor (TNF)  
 CC receptor. The extracellular domains of BR43x2 (an isoform of TACI), TACI  
 CC or BCMA (a related B cell protein) receptor contain a cysteine rich  
 CC domain, and are used for inhibiting ztnf4 activity. Ztnf4 is a TNF  
 CC ligand. They may also be used for inhibiting BR43x2, TACI or BCMA  
 CC receptor-ligand engagement associated with activated or resting B  
 CC lymphocytes effector T-cells, or with antibody production. The antibody  
 CC production is associated with an autoimmune disease selected from  
 CC systemic lupus erythematosus, myasthenia gravis, multiple sclerosis and  
 CC rheumatoid arthritis. The ztnf4 activity and BR43x2, TACI or BCMA  
 CC receptor-ligand engagement is associated with asthma, bronchitis,  
 CC emphysema, end stage renal failure, glomerulonephritis, vasculitis,  
 CC



CC nephritis, pyelonephritis, renal neoplasms, multiple myelomas, lymphomas,  
CC light chain neuropathy, amyloidosis, moderating immune response,  
CC immunosuppression, graft rejection, graft versus host disease,  
CC inflammation, insulin dependent diabetes mellitus, Crohn's disease, joint  
CC pain, swelling, anaemia, or septic shock. BR43x2, TACI, and BCMA  
CC polypeptides, fusions, antibodies, agonists or antagonists can be used to  
CC treat hypertension, renal artery stenosis, or occlusion, and cholesterol  
CC or renal emboli  
XX  
SQ Sequence 293 AA;  
Query Match 100.0%; Score 315; DB 3; Length 293;  
Best Local Similarity 100.0%; Pred. No. 1e-32;  
Matches 62; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 ENKLSPVNLPPELRRQSGEVENNSDGRYQGLEHRCSEASPALPGLKLSADQVALVY 60  
Db 105 ENKLSPVNLPPELRRQSGEVENNSDGRYQGLEHRCSEASPALPGLKLSADQVALVY 164  
QY 61 ST 62  
Db 165 ST 166  
RESULT 12  
AAE09240  
ID AAE09240 standard; protein; 293 AA.  
AC AAE09240;  
XX  
DT 19-NOV-2001 (first entry)  
DE Human TACI protein.  
XX  
KW Human; TNF; tumour necrosis factor; TALL-1; APRIL; TNF receptor; TNFR;  
KW TACI; BCMA; therapy; cancer; leukaemia; myeloma; lymphoma;  
KW autoimmune disease; rheumatoid arthritis; multiple sclerosis; psoriasis.  
XX  
OS Homo sapiens.  
XX  
PN WO200160397-A1.  
XX  
PD 23-AUG-2001.  
XX  
PF 28-NOV-2000; 2000WO-US032378.  
XX  
PR 16-FEB-2000; 2000US-0182938P.  
PR 22-AUG-2000; 2000US-0226986P.  
XX  
PA (GETH ) GENENTECH INC.  
XX  
PI Ashkenazi AJ, Dodge KH, Grewal I, Kim KJ, Marsters SA, Pitti RM;  
PI Yan M;  
XX  
DR WPI; 2001-541628/60.  
DR N-PSDB; AAD15901.  
XX  
PT Inhibiting or neutralizing TALL-1 or APRIL polypeptide biological  
PT activity, for treating autoimmune disorders and cancer, comprises  
PT exposing the cells to TALL-1 or APRIL polypeptide agonists or  
PT antagonists.  
XX  
PS Example 1; Fig 1; 160pp; English.  
XX  
CC The invention relates to methods of using one or more agonists or  
CC antagonists to modulate the activity of the members of TNF (tumour  
CC necrosis factor) especially TALL-1, APRIL and TNF receptor (TNFR) e.g.  
CC TACI or BCMA. The method is useful for treating pathological conditions  
CC or diseases associated with increased TALL-1 and APRIL expression or  
CC activity. TALL-1 and APRIL antagonists are used to block the interaction  
CC between APRIL and TALL-1 with TACI or BCMA. They are useful for treating  
CC a mammal suffering from cancer such as leukaemia, lymphoma, myeloma,  
CC cancers of lung and colon and autoimmune diseases e.g. rheumatoid

CC arthritis, multiple sclerosis, psoriasis and lupus erythematosus. The  
CC present sequence is human TACI protein  
XX  
SQ Sequence 293 AA;  
Query Match 100.0%; Score 315; DB 4; Length 293;  
Best Local Similarity 100.0%; Pred. No. 1e-32;  
Matches 62; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 ENKLSPVNLPPELRRQSGEVENNSDGRYQGLEHRCSEASPALPGLKLSADQVALVY 60  
Db 105 ENKLSPVNLPPELRRQSGEVENNSDGRYQGLEHRCSEASPALPGLKLSADQVALVY 164  
QY 61 ST 62  
Db 165 ST 166  
RESULT 13  
AAY71914  
ID AAY71914 standard; protein; 293 AA.  
XX  
AC AAY71914;  
XX  
DT 26-MAR-2001 (first entry)  
DE Human tumour necrosis factor receptor (TACI) protein.  
XX  
KW Human; transmembrane activator and CAML interactor; TACI;  
KW tumour necrosis factor receptor; TNF; autoimmune disease; diabetes;  
KW calcium-signal modulating cyclophilin ligand; CAML; viral infection;  
KW neutrokin alpha polypeptide; TACI-Ligand; TACI-L; cytostatic; therapy;  
KW neuroprotective; antidiabetic; antiviral; antiinflammatory; tumour;  
KW antiarthritic; antirheumatic; immunosuppressive; multiple sclerosis;  
KW rheumatoid arthritis; graft rejection; inflammation; cell proliferation;  
KW cell death; immunoglobulin E-mediated allergic reaction; IgE.  
XX  
OS Homo sapiens.  
XX  
FH Key Location/Qualifiers  
FT Domain 2..166  
FT /label= Extracellular domain  
FT /note= "Binds with amino acids 123-285 of extracellular  
FT domain of TACI-L"  
XX  
PN WO200067034-A1.  
XX  
PD 09-NOV-2000.  
XX  
PF 14-APR-2000; 2000WO-US010282.  
XX  
PR 30-APR-1999; 99US-00302863.  
XX  
PA (IMMV ) IMMUNEX CORP.  
XX  
PI Goodwin RG, Din WS;  
PI  
XX  
XX WPI; 2001-016005/02.  
DR N-PSDB; AAD02006.  
XX  
PT Use of new interactions between tumor necrosis factor receptors (TACI)  
PT and TACI ligands to screen candidate molecules for determining agonist  
PT and antagonist interactions which are used for treating inflammation.  
XX  
PS Claim 10; Fig 1b; 45pp; English.  
XX  
CC The present sequence is a human tumour necrosis factor receptor (TACI)  
CC protein. TACI (Transmembrane activator and calcium-signal modulating  
CC cyclophilin ligand (CAML)-interactor) forms a complex with neutrokin  
CC alpha polypeptide (TACI-Ligand). The antagonist or agonist of TACI/TACI-L  
CC complex is useful for modulating an intracellular signalling cascade  
CC mediated by TACI/TACI-L complex. Antagonists of TACI/TACI-L complex are  
CC used to inhibit the interaction between TACI and TACI-L for therapeutic

CC purposes to treat tumour and tumour metastasis and to combat various  
 CC autoimmune diseases e.g. multiple sclerosis and diabetes, as well as  
 CC other disorders, such as viral infection, rheumatoid arthritis, graft  
 CC rejection, and immunoglobulin (Ig) E-mediated allergic reactions and  
 CC inflammation. The interaction is used to study cellular processes  
 CC associated with tumour necrosis factor (TNF)-receptors such as immune  
 CC regulation, cell proliferation, cell death and inflammatory responses.  
 CC The interaction between the extracellular region of TACI and TACI-L can  
 CC be used to further develop understanding of which cell types TACI-L acts  
 CC upon  
 XX  
 SQ Sequence 293 AA;

Query Match 100.0%; Score:315; DB 4; Length 293;  
 Best Local Similarity 100.0%; Pred. No. 1e-32;  
 Matches 62; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 ENKLRSPVNLPPELRRQSGEVENNSDNGRYQGLEHRSSEASPALPGLKLSADQVALVY 60  
 DB |||||  
 105 ENKLRSPVNLPPELRRQSGEVENNSDNGRYQGLEHRSSEASPALPGLKLSADQVALVY 164  
 QY 61 ST 62  
 ||  
 DB 165 ST 166

RESULT 14  
 AAO14130  
 ID AAO14130 standard; protein; 293 AA.  
 XX  
 AC AAO14130;  
 DT 02-MAY-2002 (first entry)  
 DE Human transmembrane activator CAML interactor protein (TACI).  
 XX  
 KW Human transmembrane activator CAML interactor protein; TACI; cytostatic;  
 KW cell proliferation; tumour; vulvar; renal cell cancer; mastocytoma;  
 KW Kaposi's sarcoma; breast; ovarian carcinoma; rectal; throat; melanoma;  
 KW colon; bladder; mammary adenocarcinoma; gastrointestinal; hyperplasia;  
 KW pharyngeal squamous cell; stomach; cellular hyperproliferation; pannus;  
 KW scleroderma; rheumatoid arthritis; scarring; liver; lung fibrosis;  
 KW uterine.  
 XX  
 OS Homo sapiens.  
 XX  
 FH Key Location/Qualifiers  
 FT Domain 1..114  
 FT /label= Extracellular\_domain  
 XX  
 PN WO200181417-A2.  
 XX  
 PD 01-NOV-2001.  
 XX  
 XX 27-APR-2001; 2001WO-US040626.  
 XX  
 XX 27-APR-2000; 2000US-0199946P.  
 XX  
 XX (BIOJ) BIOGEN INC.  
 XX (APOT-) APOTEC R & D SA.  
 XX  
 PI Ambrose C, Thompson J, Schneider P, Rennert P;  
 XX  
 DR WPI; 2002-062027/08.  
 DR N-PSDB; AAK98726.  
 XX  
 XX Treating mammal for condition associated with undesired cell  
 XX proliferation e.g., solid tumor or reducing solid tumor size located in  
 XX mammal comprises administering transmembrane activator CAML interactor  
 XX protein reagent.  
 XX  
 XX Claim 8; Fig 1; 42pp; English.  
 PS  
 XX

CC This sequence represents the human transmembrane activator CAML  
 CC interactor protein (TACI). The invention relates to treating a mammal for  
 CC a condition associated with undesired cell proliferation (e.g. a solid  
 CC tumour, or reducing the size of a solid tumour located on or in a mammal)  
 CC comprising administering a transmembrane activator CAML interactor  
 CC protein (TACI) reagent. The TACI reagent has cytostatic and vulnarary  
 CC activity. Treating a mammal (e.g. human, cow, horse, dog, mouse, rat or  
 CC cat) for a condition associated with undesired cell proliferation (e.g.  
 CC cancer such as renal cell cancer, Kaposi's sarcoma, breast cancer,  
 CC sarcoma, ovarian carcinoma, rectal cancer, throat cancer, melanoma, colon  
 CC cancer, bladder cancer, mastocytoma, lung cancer, mammary adenocarcinoma,  
 CC pharyngeal squamous cell carcinoma, gastrointestinal cancer or stomach  
 CC cancer). The method is also useful for treating cellular  
 CC hyperproliferation (hyperplasia) such as scleroderma, pannus formation in  
 CC rheumatoid arthritis, post-surgical scarring and lung, liver and uterine  
 CC fibrosis. The TACI reagent of the invention can extend mean survival time  
 CC of a mammal by 25% as compared to the mean survival time of a mammal in  
 CC the absence of administering the TACI reagent. The TACI reagent also  
 CC reduces the size of the tumour by 25% or more  
 XX  
 SQ Sequence 293 AA;

Query Match 100.0%; Score 315; DB 5; Length 293;  
 Best Local Similarity 100.0%; Pred. No. 1e-32;  
 Matches 62; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 ENKLRSPVNLPPELRRQSGEVENNSDNGRYQGLEHRSSEASPALPGLKLSADQVALVY 60  
 DB |||||  
 105 ENKLRSPVNLPPELRRQSGEVENNSDNGRYQGLEHRSSEASPALPGLKLSADQVALVY 164  
 QY 61 ST 62  
 ||  
 DB 165 ST 166

RESULT 15  
 ABB81488  
 ID ABB81488 standard; protein; 293 AA.  
 XX  
 AC ABB81488;  
 XX  
 DT 02-SEP-2002 (first entry)  
 DE Human TACI receptor related protein SEQ ID NO:8.  
 XX  
 KW Human; Tnfr12; tumour necrosis factor receptor; cytostatic;  
 KW immunosuppressive; dermatological; antiinflammatory; antidiabetic;  
 KW neuroprotective; antirheumatic; antiarthritic; antiasthmatic;  
 KW nephrotropic; hypotensive; gene therapy; B lymphocyte; tumour;  
 KW autoimmune disorder; systemic lupus erythematosus; myasthenia gravis;  
 KW multiple sclerosis; insulin dependent diabetes mellitus; asthma;  
 KW rheumatoid arthritis; bronchitis; emphysema; renal disease; lymphoma;  
 KW glomerulonephritis; vasculitis; chronic lymphoid leukaemia; nephritis;  
 KW pyelonephritis; renal neoplasm; multiple myeloma; amyloidosis;  
 KW light chain neuropathy; hypertension; large vessel disease;  
 KW graft-versus host disease; graft rejection; Crohn's disease.  
 XX  
 OS Homo sapiens.  
 XX  
 XX WO200238766-A2.  
 XX  
 PD 16-MAY-2002.  
 XX  
 XX 05-NOV-2001; 2001WO-US047018.  
 XX  
 XX 07-NOV-2000; 2000US-0246449P.  
 XX  
 XX 20-DEC-2000; 2000US-0257131P.  
 XX  
 XX 28-JUN-2001; 2001US-0301715P.  
 XX  
 XX 29-AUG-2001; 2001US-0315565P.  
 XX  
 XX (ZYMO) ZYMOGENETICS INC.  
 XX  
 XX Gross JA, Xu W, Henne RM, Grant FJ;

XX WPI; 2002-508212/54.  
DR  
XX  
PT Novel isolated human tumor necrosis factor receptor polypeptide, termed  
PT Ztnfr 12, useful for treating autoimmune disorders, emphysema, end stage  
PT renal failure or renal disease and lymphoma.  
XX  
XX  
PS Disclosure; Page 136-137; 154pp; English.  
XX  
XX The present invention describes a human tumour necrosis factor receptor  
CC designated Ztnfr12 (I). (I) has cytostatic, immunosuppressive,  
CC dermatological, antiinflammatory, neuroprotective, antidiabetic,  
CC antirheumatic, antiarthritic, antiasthmatic, nephrotropic and hypotensive  
CC activities, and can be used in gene therapy. (I) can be used for  
CC inhibiting, in a mammal, the activity of a ligand that binds Ztnfr12  
CC (e.g. ZTNF4), for treating disorders and diseases associated with B  
CC lymphocytes, activated B lymphocytes or resting B lymphocytes, and for  
CC inhibiting the proliferation of tumour cells. (I) is useful for treating  
CC autoimmune disorders such as systemic lupus erythematosus, myasthenia  
CC gravis, multiple sclerosis, insulin dependent diabetes mellitus, asthma,  
CC rheumatoid arthritis, bronchitis, emphysema and end stage renal failure  
CC or renal disease such as glomerulonephritis, vasculitis, chronic lymphoid  
CC leukaemia, nephritis, and pyelonephritis, and for treating renal  
CC neoplasms, multiple myelomas, lymphomas, light chain neuropathy, or  
CC amyloidosis, hypertension, large vessel diseases, graft-versus host  
CC disease, graft rejection and Crohn's disease. (I) is useful for  
CC modulating the immune system, for regulating B cell responses and  
CC development, for modulating development of other cells, antibody  
CC production and cytokine production, and for modulating T and B cell  
CC communication. The present sequence represents a protein which is given  
CC in the exemplification of the present invention  
XX  
SQ Sequence 293 AA;

Query Match 100.0%; Score 315; DB 5; Length 293;  
Best Local Similarity 100.0%; Pred. No. 1e-32;  
Matches 62; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
  
QY 1 ENKLSPVNLPELRRQRSGEVENNSDNGRYQGLEHRCSEASPALPGLKLSADQVALVY 60  
Db 105 ENKLSPVNLPELRRQRSGEVENNSDNGRYQGLEHRCSEASPALPGLKLSADQVALVY 164  
  
QY 61 ST 62  
Db 165 ST 166

Search completed: November 19, 2004, 23:40:02  
Job time : 114.028 secs

**This Page Blank (uspto)**

GenCore version 5.1.6  
Copyright (c) 1993 - 2004 Compugen Ltd.

OM protein - protein search, using sw model

Run on: November 19, 2004, 23:37:09 ; Search time 48.9014 Seconds  
(without alignments)  
84.082 Million cell updates/sec

Title: US-10-068-725-4\_COPY\_105\_166

Perfect score: 315

Sequence: 1 ENKLSPVNLPELRRQSG.....SPALPGLKLSADQVALVYST 62

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 478139 seqs, 63118000 residues

Total number of hits satisfying chosen parameters: 478139

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Issued Patents AA.\*

1: /cgn2\_6/prodata/1/1aa/5A-COMB.pep.\*  
2: /cgn2\_6/prodata/1/1aa/5B-COMB.pep.\*  
3: /cgn2\_6/prodata/1/1aa/6A-COMB.pep.\*  
4: /cgn2\_6/prodata/1/1aa/6B-COMB.pep.\*  
5: /cgn2\_6/prodata/1/1aa/PCTUS-COMB.pep.\*  
6: /cgn2\_6/prodata/1/1aa/backfiles1.pep.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

| Result No. | Score | Query Match | Length | ID | Description          |
|------------|-------|-------------|--------|----|----------------------|
| 1          | 315   | 100.0       | 166    | 2  | US-08-810-572A-6     |
| 2          | 315   | 100.0       | 166    | 3  | US-09-290-333-6      |
| 3          | 315   | 100.0       | 166    | 4  | US-09-782-857A-6     |
| 4          | 315   | 100.0       | 166    | 4  | US-09-854-864-15     |
| 5          | 315   | 100.0       | 293    | 2  | US-08-810-572A-2     |
| 6          | 315   | 100.0       | 293    | 3  | US-09-290-333-2      |
| 7          | 315   | 100.0       | 293    | 4  | US-09-782-857A-2     |
| 8          | 315   | 100.0       | 293    | 4  | US-09-879-919-22     |
| 9          | 315   | 100.0       | 293    | 4  | US-09-848-295-4      |
| 10         | 315   | 100.0       | 293    | 4  | US-09-854-864-14     |
| 11         | 310   | 98.4        | 397    | 4  | US-09-854-864-18     |
| 12         | 66    | 21.0        | 428    | 4  | US-09-252-991A-24431 |
| 13         | 64    | 20.3        | 328    | 4  | US-09-252-991A-23205 |
| 14         | 64    | 20.3        | 341    | 4  | US-09-252-991A-18308 |
| 15         | 62    | 19.7        | 179    | 4  | US-09-252-991A-30669 |
| 16         | 62    | 19.7        | 635    | 4  | US-09-252-991A-21514 |
| 17         | 62    | 19.7        | 806    | 1  | US-07-980-528-2      |
| 18         | 62    | 19.7        | 824    | 4  | US-09-538-092-1242   |
| 19         | 61    | 19.4        | 412    | 4  | US-09-252-991A-30252 |
| 20         | 61    | 19.4        | 487    | 4  | US-09-248-796A-19251 |
| 21         | 60.5  | 19.2        | 336    | 4  | US-09-252-991A-22196 |
| 22         | 60.5  | 19.2        | 954    | 4  | US-09-252-991A-32931 |
| 23         | 60    | 19.0        | 349    | 3  | US-09-343-011B-1     |
| 24         | 60    | 19.0        | 487    | 4  | US-09-252-991A-18581 |
| 25         | 59.5  | 18.9        | 203    | 4  | US-09-134-000C-6471  |
| 26         | 59    | 18.7        | 242    | 4  | US-09-270-767-43590  |
| 27         | 59    | 18.7        | 710    | 3  | US-09-079-812E-2     |

|    |      |      |      |   |                      |                   |
|----|------|------|------|---|----------------------|-------------------|
| 28 | 58.5 | 18.6 | 214  | 4 | US-09-252-991A-22902 | Sequence 22902, A |
| 29 | 58.5 | 18.6 | 261  | 4 | US-09-252-991A-28545 | Sequence 28545, A |
| 30 | 58.5 | 18.6 | 453  | 4 | US-09-270-767-44670  | Sequence 44670, A |
| 31 | 58.5 | 18.6 | 693  | 4 | US-09-252-991A-24059 | Sequence 24059, A |
| 32 | 58   | 18.4 | 511  | 4 | US-09-198-452A-509   | Sequence 509, App |
| 33 | 58   | 18.4 | 621  | 3 | US-09-026-343-7      | Sequence 7, Appli |
| 34 | 58   | 18.4 | 621  | 3 | US-09-362-871-7      | Sequence 7, Appli |
| 35 | 58   | 18.4 | 1385 | 2 | US-08-687-399-7      | Sequence 7, Appli |
| 36 | 57.5 | 18.3 | 190  | 4 | US-09-270-767-46639  | Sequence 46639, A |
| 37 | 57.5 | 18.3 | 362  | 4 | US-09-252-991A-30223 | Sequence 30223, A |
| 38 | 57.5 | 18.3 | 385  | 4 | US-09-252-991A-25080 | Sequence 25080, A |
| 39 | 57.5 | 18.3 | 584  | 4 | US-09-270-767-43419  | Sequence 43419, A |
| 40 | 57   | 18.1 | 179  | 4 | US-09-252-991A-25298 | Sequence 25298, A |
| 41 | 57   | 18.1 | 213  | 4 | US-09-252-991A-32093 | Sequence 32093, A |
| 42 | 57   | 18.1 | 230  | 4 | US-09-252-991A-17268 | Sequence 17268, A |
| 43 | 57   | 18.1 | 258  | 4 | US-09-252-991A-31620 | Sequence 31620, A |
| 44 | 57   | 18.1 | 430  | 1 | US-08-035-392-4      | Sequence 4, Appli |
| 45 | 57   | 18.1 | 430  | 1 | US-08-504-511A-4     | Sequence 4, Appli |

## ALIGNMENTS

## RESULT 1

US-08-810-572A-6  
; Sequence 6, Application US/08810572A  
; Patent No. 5969102

; GENERAL INFORMATION:

; APPLICANT: Bram, Richard J.

; APPLICANT: von Bulow, Gotz

; TITLE OF INVENTION: A LYMPHOCYTE SURFACE RECEPTOR THAT BINDS

; TITLE OF INVENTION: CAML, NUCLEIC ACIDS ENCODING THE SAME AND METHODS OF USE

; NUMBER OF SEQUENCES: 11

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: David A. Jackson, Esq.

; STREET: 411 Hackensack Ave, Continental Plaza, 4th

; STREET: Floor

; CITY: Hackensack

; STATE: New Jersey

; COUNTRY: USA

; ZIP: 07601

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

; COMPUTER: IBM PC compatible

; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: Patent In Release #1.0, Version #1.30

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/08/810,572A

; FILING DATE: 28-FEB-1997

; CLASSIFICATION: 536

; ATTORNEY/AGENT INFORMATION:

; NAME: Jackson Esq., David A.

; REGISTRATION NUMBER: 26,742

; REFERENCE/DOCKET NUMBER: 1340-1-007

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: 201-487-5800

; TELEFAX: 201-343-1684

; INFORMATION FOR SEQ ID NO: 6:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 166 amino acids

; TYPE: amino acid

; STRANDEDNESS: single

; TOPOLOGY: linear

; MOLECULE TYPE: peptide

; HYPOTHETICAL: NO

; FRAGMENT TYPE: N-terminal

; ORIGINAL SOURCE:

; ORGANISM: Homo sapiens

; US-08-810-572A-6

Query Match 100.0%; Score 315; DB 2; Length 166;

Best Local Similarity 100.0%; Pred. No. 7.1e-34;

Sun Nov 21 13:23:27 2004

Matches 62; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ENKLRSPVNLPPPLRQRSGEVENNSGRYQGLEHGRSEASPALPGLKLSADQVALVY 60  
 Db 105 ENKLRSPVNLPPPLRQRSGEVENNSGRYQGLEHGRSEASPALPGLKLSADQVALVY 164

Qy 61 ST 62  
 Db 165 ST 166

RESULT 2  
 US-09-290-333-6  
 ; Sequence 6, Application US/09290333  
 ; Patent No. 6316222  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Bram, Richard J.  
 ; von Bulow, Gotz  
 ; TITLE OF INVENTION: A LYMPHOCYTE SURFACE RECEPTOR THAT BINDS  
 ; CAML, NUCLEIC ACIDS ENCODING THE SAME AND METHODS OF USE  
 ; THEREOF  
 ; NUMBER OF SEQUENCES: 11  
 ; CORRESPONDENCE ADDRESS:  
 ; ADDRESSEE: David A. Jackson, Esq.  
 ; STREET: 411 Hackensack Ave, Continental Plaza, 4th  
 ; Floor  
 ; CITY: Hackensack  
 ; STATE: New Jersey  
 ; COUNTRY: USA  
 ; ZIP: 07601  
 ; COMPUTER READABLE FORM:  
 ; MEDIUM TYPE: Floppy disk  
 ; COMPUTER: IBM PC compatible  
 ; OPERATING SYSTEM: PC-DOS/MS-DOS  
 ; SOFTWARE: Patent In Release #1.0, Version #1.30  
 ; CURRENT APPLICATION DATA:  
 ; APPLICATION NUMBER: US/09/290,333  
 ; FILING DATE: 12-Apr-1999  
 ; CLASSIFICATION: <Unknown>  
 ; ATTORNEY/AGENT INFORMATION:  
 ; NAME: Jackson Esq., David A.  
 ; REGISTRATION NUMBER: 26,742  
 ; REFERENCE/DOCKET NUMBER: 1340-1-007 PCT  
 ; TELECOMMUNICATION INFORMATION:  
 ; TELEPHONE: 201-487-5800  
 ; TELEFAX: 201-343-1684  
 ; INFORMATION FOR SEQ ID NO: 6:  
 ; SEQUENCE CHARACTERISTICS:  
 ; LENGTH: 166 amino acids  
 ; TYPE: amino acid  
 ; STRANDEDNESS: single  
 ; TOPOLOGY: linear  
 ; MOLECULE TYPE: peptide  
 ; HYPOTHETICAL: NO  
 ; FRAGMENT TYPE: N-terminal  
 ; ORIGINAL SOURCE:  
 ; ORGANISM: Homo sapiens  
 ; SEQUENCE DESCRIPTION: SEQ ID NO: 6:  
 ; US-09-290-333-6

Query Match 100.0%; Score 315; DB 3; Length 166;  
 Best Local Similarity 100.0%; Pred. No. 7,1e-34;  
 Matches 62; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ENKLRSPVNLPPPLRQRSGEVENNSGRYQGLEHGRSEASPALPGLKLSADQVALVY 60  
 Db 105 ENKLRSPVNLPPPLRQRSGEVENNSGRYQGLEHGRSEASPALPGLKLSADQVALVY 164

Qy 61 ST 62  
 Db 165 ST 166

RESULT 3  
 US-09-782-857A-6  
 ; Sequence 6, Application US/09782857A  
 ; Patent No. 6500428  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Bram, Richard J.  
 ; von Bulow, Gotz  
 ; TITLE OF INVENTION: A LYMPHOCYTE SURFACE RECEPTOR THAT BINDS  
 ; CAML, NUCLEIC ACIDS ENCODING THE SAME AND METHODS OF USE  
 ; THEREOF  
 ; NUMBER OF SEQUENCES: 10  
 ; CORRESPONDENCE ADDRESS:  
 ; ADDRESSEE: David A. Jackson, Esq.  
 ; STREET: 411 Hackensack Ave, Continental Plaza, 4th  
 ; Floor  
 ; CITY: Hackensack  
 ; STATE: New Jersey  
 ; COUNTRY: USA  
 ; ZIP: 07601  
 ; COMPUTER READABLE FORM:  
 ; MEDIUM TYPE: Floppy disk  
 ; COMPUTER: IBM PC compatible  
 ; OPERATING SYSTEM: PC-DOS/MS-DOS  
 ; SOFTWARE: Patent In Release #1.0, Version #1.30  
 ; CURRENT APPLICATION DATA:  
 ; APPLICATION NUMBER: US/09/782,857A  
 ; FILING DATE: 14-Feb-2001  
 ; CLASSIFICATION: <Unknown>  
 ; PRIOR APPLICATION DATA:  
 ; APPLICATION NUMBER: 08/810,572  
 ; FILING DATE: <Unknown>  
 ; ATTORNEY/AGENT INFORMATION:  
 ; NAME: Jackson Esq., David A.  
 ; REGISTRATION NUMBER: 26,742  
 ; REFERENCE/DOCKET NUMBER: 1340-1-007  
 ; TELECOMMUNICATION INFORMATION:  
 ; TELEPHONE: 201-487-5800  
 ; TELEFAX: 201-343-1684  
 ; INFORMATION FOR SEQ ID NO: 6:  
 ; SEQUENCE CHARACTERISTICS:  
 ; LENGTH: 166 amino acids  
 ; TYPE: amino acid  
 ; STRANDEDNESS: single  
 ; TOPOLOGY: linear  
 ; MOLECULE TYPE: peptide  
 ; HYPOTHETICAL: NO  
 ; FRAGMENT TYPE: N-terminal  
 ; ORIGINAL SOURCE:  
 ; ORGANISM: Homo sapiens  
 ; SEQUENCE DESCRIPTION: SEQ ID NO: 6:  
 ; US-09-782-857A-6

Query Match 100.0%; Score 315; DB 4; Length 166;  
 Best Local Similarity 100.0%; Pred. No. 7,1e-34;  
 Matches 62; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ENKLRSPVNLPPPLRQRSGEVENNSGRYQGLEHGRSEASPALPGLKLSADQVALVY 60  
 Db 105 ENKLRSPVNLPPPLRQRSGEVENNSGRYQGLEHGRSEASPALPGLKLSADQVALVY 164

Qy 61 ST 62  
 Db 165 ST 166

RESULT 4  
 US-09-854-864-15  
 ; Sequence 15, Application US/09854864  
 ; Patent No. 6774106  
 ; GENERAL INFORMATION:  
 ; APPLICANT: THEILL, LARS EYDE  
 ; APPLICANT: YU, GANG  
 ; TITLE OF INVENTION: METHODS AND COMPOSITIONS OF MATTER CONCERNING APRIL/G70, BCMA,

```
; TITLE OF INVENTION: BLYS/AGP-3, AND TAC1
; FILE REFERENCE: A-686B
; CURRENT APPLICATION NUMBER: US/09/854,864
; PRIOR FILING DATE: 2001-09-11
; PRIOR APPLICATION NUMBER: US 60/204,039
; PRIOR FILING DATE: 2000-05-12
; PRIOR APPLICATION NUMBER: US 60/214,591
; PRIOR FILING DATE: 2000-06-27
; NUMBER OF SEQ ID NOS: 31
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 15
; LENGTH: 166
; TYPE: PRT
; ORGANISM: Homo sapiens
; US-09-854-864-15

Query Match      100.0%; Score 315; DB 4; Length 166;
Best Local Similarity 100.0%; Pred. No. 7.1e-34; Indels 0; Gaps 0;
Matches 62; Conservative 0; Mismatches 0;

QY 1 ENKLSPVNLPPELRRQSRGSEVNNDSNGRYQGLEHGRSEASPALPGLKLSADQVALVY 60
   |||||
Db 105 ENKLSPVNLPPELRRQSRGSEVNNDSNGRYQGLEHGRSEASPALPGLKLSADQVALVY 164

QY 61 ST 62
Db 165 ST 166

RESULT 5
US-08-810-572A-2
; Sequence 2, Application US/08810572A
; Patent No. 5969102
; GENERAL INFORMATION:
; APPLICANT: Bram, Richard J.
; APPLICANT: von Bulow, Gotz
; TITLE OF INVENTION: A LYMPHOCYTE SURFACE RECEPTOR THAT BINDS
; TITLE OF INVENTION: CAML, NUCLEIC ACIDS ENCODING THE SAME AND METHODS OF USE
; NUMBER OF SEQUENCES: 11
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: David A. Jackson, Esq.
; STREET: 411 Hackensack Ave, Continental Plaza, 4th
; FLOOR:
; CITY: Hackensack
; STATE: New Jersey
; COUNTRY: USA
; ZIP: 07601
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/810,572A
; FILING DATE: 28-FEB-1997
; CLASSIFICATION: 536
; ATTORNEY/AGENT INFORMATION:
; NAME: Jackson Esq., David A.
; REGISTRATION NUMBER: 26,742
; REFERENCE/DOCKET NUMBER: 1340-1-007
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 201-487-5800
; TELEFAX: 201-343-1684
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 293 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; HYPOTHETICAL: NO
; FRAGMENT TYPE: N-terminal

QY 1 ENKLSPVNLPPELRRQSRGSEVNNDSNGRYQGLEHGRSEASPALPGLKLSADQVALVY 60
   |||||
Db 105 ENKLSPVNLPPELRRQSRGSEVNNDSNGRYQGLEHGRSEASPALPGLKLSADQVALVY 164
```

```
; ORIGINAL SOURCE:
; ORGANISM: Homo sapiens
; US-08-810-572A-2

Query Match      100.0%; Score 315; DB 2; Length 293;
Best Local Similarity 100.0%; Pred. No. 1.5e-33;
Matches 62; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ENKLSPVNLPPELRRQSRGSEVNNDSNGRYQGLEHGRSEASPALPGLKLSADQVALVY 60
   |||||
Db 105 ENKLSPVNLPPELRRQSRGSEVNNDSNGRYQGLEHGRSEASPALPGLKLSADQVALVY 164

QY 61 ST 62
Db 165 ST 166

RESULT 6
US-09-290-333-2
; Sequence 2, Application US/09290333
; Patent No. 6316222
; GENERAL INFORMATION:
; APPLICANT: Bram, Richard J.
; APPLICANT: von Bulow, Gotz
; TITLE OF INVENTION: A LYMPHOCYTE SURFACE RECEPTOR THAT BINDS
; TITLE OF INVENTION: CAML, NUCLEIC ACIDS ENCODING THE SAME AND METHODS OF USE
; THEREOF
; NUMBER OF SEQUENCES: 11
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: David A. Jackson, Esq.
; STREET: 411 Hackensack Ave, Continental Plaza, 4th
; FLOOR:
; CITY: Hackensack
; STATE: New Jersey
; COUNTRY: USA
; ZIP: 07601
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/290,333
; FILING DATE: 12-Apr-1999
; CLASSIFICATION: <Unknown>
; ATTORNEY/AGENT INFORMATION:
; NAME: Jackson Esq., David A.
; REGISTRATION NUMBER: 26,742
; REFERENCE/DOCKET NUMBER: 1340-1-007 PCT
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 201-487-5800
; TELEFAX: 201-343-1684
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 293 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; HYPOTHETICAL: NO
; FRAGMENT TYPE: N-terminal
; ORIGINAL SOURCE:
; ORGANISM: Homo sapiens
; SEQUENCE DESCRIPTION: SEQ ID NO: 2:
; US-09-290-333-2

Query Match      100.0%; Score 315; DB 3; Length 293;
Best Local Similarity 100.0%; Pred. No. 1.5e-33;
Matches 62; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ENKLSPVNLPPELRRQSRGSEVNNDSNGRYQGLEHGRSEASPALPGLKLSADQVALVY 60
   |||||
Db 105 ENKLSPVNLPPELRRQSRGSEVNNDSNGRYQGLEHGRSEASPALPGLKLSADQVALVY 164
```





Db 105 ENKLRSPVNLPELRRQRSGEVENNSDNGRYQGLEHRGSEASPALPGLKLSADQVALVY 164  
QY 61 ST 62  
Db 165 ST 166

RESULT 10  
US-09-854-864-14  
; Sequence 14, Application US/09854864  
; Patent No. 6774106  
; GENERAL INFORMATION:  
; APPLICANT: THEILL, LARS EYDE  
; APPLICANT: YU, GANG  
; TITLE OF INVENTION: METHODS AND COMPOSITIONS OF MATTER CONCERNING APRIL/G70, BCMA,  
; FILE REFERENCE: A-686B  
; CURRENT APPLICATION NUMBER: US/09/854,864  
; CURRENT FILING DATE: 2001-09-11  
; PRIOR APPLICATION NUMBER: US 60/204,039  
; PRIOR FILING DATE: 2000-05-12  
; PRIOR APPLICATION NUMBER: US 60/214,591  
; PRIOR FILING DATE: 2000-06-27  
; NUMBER OF SEQ ID NOS: 31  
; SOFTWARE: PatentIn version 3.1  
; SEQ ID NO 14  
; LENGTH: 293  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-09-854-864-14

Query Match 100.0%; Score 315; DB 4; Length 293;  
Best Local Similarity 100.0%; Pred. No. 1.5e-33;  
Matches 62; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ENKLRSPVNLPELRRQRSGEVENNSDNGRYQGLEHRGSEASPALPGLKLSADQVALVY 60  
Db 105 ENKLRSPVNLPELRRQRSGEVENNSDNGRYQGLEHRGSEASPALPGLKLSADQVALVY 164  
QY 61 ST 62  
Db 165 ST 166

RESULT 11  
US-09-854-864-18  
; Sequence 18, Application US/09854864  
; Patent No. 6774106  
; GENERAL INFORMATION:  
; APPLICANT: THEILL, LARS EYDE  
; APPLICANT: YU, GANG  
; TITLE OF INVENTION: METHODS AND COMPOSITIONS OF MATTER CONCERNING APRIL/G70, BCMA,  
; FILE REFERENCE: A-686B  
; CURRENT APPLICATION NUMBER: US/09/854,864  
; CURRENT FILING DATE: 2001-09-11  
; PRIOR APPLICATION NUMBER: US 60/204,039  
; PRIOR FILING DATE: 2000-05-12  
; PRIOR APPLICATION NUMBER: US 60/214,591  
; PRIOR FILING DATE: 2000-06-27  
; NUMBER OF SEQ ID NOS: 31  
; SOFTWARE: PatentIn version 3.1  
; SEQ ID NO 18  
; LENGTH: 397  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-09-854-864-18

Query Match 98.4%; Score 310; DB 4; Length 397;  
Best Local Similarity 100.0%; Pred. No. 1e-32;  
Matches 61; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ENKLRSPVNLPELRRQRSGEVENNSDNGRYQGLEHRGSEASPALPGLKLSADQVALVY 60

Db 105 ENKLRSPVNLPELRRQRSGEVENNSDNGRYQGLEHRGSEASPALPGLKLSADQVALVY 164  
QY 61 S 61  
Db 165 S 165

RESULT 12  
US-09-252-991A-24431  
; Sequence 24431, Application US/09252991A  
; Patent No. 6551795  
; GENERAL INFORMATION:  
; APPLICANT: Marc J. Rubenfield et al.  
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS  
; FILE REFERENCE: 107196.136  
; CURRENT APPLICATION NUMBER: US/09/252,991A  
; CURRENT FILING DATE: 1999-02-18  
; PRIOR APPLICATION NUMBER: US 60/074,788  
; PRIOR FILING DATE: 1998-02-18  
; PRIOR APPLICATION NUMBER: US 60/094,190  
; PRIOR FILING DATE: 1998-07-27  
; NUMBER OF SEQ ID NOS: 33142  
; SEQ ID NO 24431  
; LENGTH: 428  
; TYPE: PRT  
; ORGANISM: Pseudomonas aeruginosa  
US-09-252-991A-24431

Query Match 21.0%; Score 66; DB 4; Length 428;  
Best Local Similarity 40.9%; Pred. No. 2.3;  
Matches 18; Conservative 8; Mismatches 8; Indels 10; Gaps 2;

QY 14 LRRQRSGEVENNSDNGRYQGLEHRGSEASPALPGLKLSADQVA 57  
Db 254 LAQQAGHROQH-----HEGLE-----BAHPAFDLLLLAADQVA 287

RESULT 13  
US-09-252-991A-23205  
; Sequence 23205, Application US/09252991A  
; Patent No. 6551795  
; GENERAL INFORMATION:  
; APPLICANT: Marc J. Rubenfield et al.  
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS  
; FILE REFERENCE: 107196.136  
; CURRENT APPLICATION NUMBER: US/09/252,991A  
; CURRENT FILING DATE: 1999-02-18  
; PRIOR APPLICATION NUMBER: US 60/074,788  
; PRIOR FILING DATE: 1998-02-18  
; PRIOR APPLICATION NUMBER: US 60/094,190  
; PRIOR FILING DATE: 1998-07-27  
; NUMBER OF SEQ ID NOS: 33142  
; SEQ ID NO 23205  
; LENGTH: 328  
; TYPE: PRT  
; ORGANISM: Pseudomonas aeruginosa  
US-09-252-991A-23205

Query Match 20.3%; Score 64; DB 4; Length 328;  
Best Local Similarity 31.8%; Pred. No. 3;  
Matches 21; Conservative 8; Mismatches 23; Indels 14; Gaps 3;

QY 6 SPVN--LPPELRRQRSGEVENNSDNGRYQGL-----EHRGSEASPALPGLKLS 52  
Db 165 APVGAALPPAARRQRTGPA--GGGHRDGRRTALGVFALRRRDLPDFPGCARPGLOGIEQA 223  
QY 53 ADQVAL 58  
Db 224 AHRVAV 229

## RESULT 14

US-09-252-991A-18308  
; Sequence 18308, Application US/09252991A  
; Patent No. 6551795  
; GENERAL INFORMATION:  
; APPLICANT: Marc J. Rubenfield et al.  
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS  
; TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS  
; FILE REFERENCE: 107196.136  
; CURRENT APPLICATION NUMBER: US/09/252.991A  
; CURRENT FILING DATE: 1999-02-18  
; PRIOR APPLICATION NUMBER: US 60/074,788  
; PRIOR FILING DATE: 1998-02-18  
; PRIOR APPLICATION NUMBER: US 60/094,190  
; PRIOR FILING DATE: 1998-07-27  
; NUMBER OF SEQ ID NOS: 33142  
; SEQ ID NO 18308  
; LENGTH: 341  
; TYPE: PRT  
; ORGANISM: Pseudomonas aeruginosa  
US-09-252-991A-18308

Query Match 20.3%; Score 64; DB 4; Length 341;  
Best Local Similarity 30.5%; Pred. No. 3.2;  
Matches 18; Conservative 7; Mismatches 20; Indels 14; Gaps 2;  
Qy 9 NLPPELR-----QRSEVENNSDNGRYQGLEHGRSEASPALFGLKLSADQ 55  
Db 144 HLPYRRRAQRAARGPERPORTG--RHGPDRAHRRPRQHRGTAVGRLPAATVERDQ 200

## RESULT 15

US-09-252-991A-30669  
; Sequence 30669, Application US/09252991A  
; Patent No. 6551795  
; GENERAL INFORMATION:  
; APPLICANT: Marc J. Rubenfield et al.  
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS  
; TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS  
; FILE REFERENCE: 107196.136  
; CURRENT APPLICATION NUMBER: US/09/252.991A  
; CURRENT FILING DATE: 1999-02-18  
; PRIOR APPLICATION NUMBER: US 60/074,788  
; PRIOR FILING DATE: 1998-02-18  
; PRIOR APPLICATION NUMBER: US 60/094,190  
; PRIOR FILING DATE: 1998-07-27  
; NUMBER OF SEQ ID NOS: 33142  
; SEQ ID NO 30669  
; LENGTH: 179  
; TYPE: PRT  
; ORGANISM: Pseudomonas aeruginosa  
US-09-252-991A-30669

Query Match 19.7%; Score 62; DB 4; Length 179;  
Best Local Similarity 41.3%; Pred. No. 2.5;  
Matches 19; Conservative 4; Mismatches 19; Indels 4; Gaps 2;  
Qy 10 LPPELRQRSEVENNSDNGRY--QGLEHGRSEASPALFGLKLSA 53  
Db 91 LHPQLRRQRPAAHFGTTERDRRCQDQGLRRRPGSGAD--LPGLRSQA 134

Search completed: November 19, 2004, 23:45:54  
Job time : 50.9014 secs

GenCore version 5.1.6  
Copyright (c) 1993 - 2004 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: November 19, 2004, 23:40:10 ; Search time 168.535 Seconds  
(without alignments)  
130.275 Million cell updates/sec

Title: US-10-068-725-4\_COPY\_105\_166

Perfect score: 315

Sequence: 1 ENKLRSPVNLPELRQRSG.....SPALPGLKLSADQVALVYST 62

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1570615 seqs, 354127592 residues

Total number of hits satisfying chosen parameters: 1570615

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Published Applications AA:\*

- 1: /cgn2\_6/ptodata/2/pubpaa/US07\_PUBCOMB.pep.\*
- 2: /cgn2\_6/ptodata/2/pubpaa/PCT\_NEW\_PUB.pep.\*
- 3: /cgn2\_6/ptodata/2/pubpaa/US06\_NEW\_PUB.pep.\*
- 4: /cgn2\_6/ptodata/2/pubpaa/US06\_PUBCOMB.pep.\*
- 5: /cgn2\_6/ptodata/2/pubpaa/US07\_NEW\_PUB.pep.\*
- 6: /cgn2\_6/ptodata/2/pubpaa/PCTUS\_PUBCOMB.pep.\*
- 7: /cgn2\_6/ptodata/2/pubpaa/US08\_NEW\_PUB.pep.\*
- 8: /cgn2\_6/ptodata/2/pubpaa/US08\_PUBCOMB.pep.\*
- 9: /cgn2\_6/ptodata/2/pubpaa/US09A\_PUBCOMB.pep.\*
- 10: /cgn2\_6/ptodata/2/pubpaa/US09B\_PUBCOMB.pep.\*
- 11: /cgn2\_6/ptodata/2/pubpaa/US09C\_PUBCOMB.pep.\*
- 12: /cgn2\_6/ptodata/2/pubpaa/US09\_NEW\_PUB.pep.\*
- 13: /cgn2\_6/ptodata/2/pubpaa/US10A\_PUBCOMB.pep.\*
- 14: /cgn2\_6/ptodata/2/pubpaa/US10B\_PUBCOMB.pep.\*
- 15: /cgn2\_6/ptodata/2/pubpaa/US10C\_PUBCOMB.pep.\*
- 16: /cgn2\_6/ptodata/2/pubpaa/US10D\_PUBCOMB.pep.\*
- 17: /cgn2\_6/ptodata/2/pubpaa/US10\_NEW\_PUB.pep.\*
- 18: /cgn2\_6/ptodata/2/pubpaa/US11\_NEW\_PUB.pep.\*
- 19: /cgn2\_6/ptodata/2/pubpaa/US60\_NEW\_PUB.pep.\*
- 20: /cgn2\_6/ptodata/2/pubpaa/US60\_PUBCOMB.pep.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Score | Query Match | Length | ID                    | Description       |
|------------|-------|-------------|--------|-----------------------|-------------------|
| 1          | 315   | 100.0       | 166    | 9 US-09-854-864-15    | Sequence 15, Appl |
| 2          | 315   | 100.0       | 166    | 9 US-09-855-158-15    | Sequence 15, Appl |
| 3          | 315   | 100.0       | 166    | 14 US-10-293-816-6    | Sequence 6, Appl  |
| 4          | 315   | 100.0       | 293    | 9 US-09-879-919-22    | Sequence 22, Appl |
| 5          | 315   | 100.0       | 293    | 9 US-09-854-864-14    | Sequence 14, Appl |
| 6          | 315   | 100.0       | 293    | 9 US-09-855-158-14    | Sequence 14, Appl |
| 7          | 315   | 100.0       | 293    | 9 US-09-961-376-2     | Sequence 2, Appl  |
| 8          | 315   | 100.0       | 293    | 9 US-09-779-050A-42   | Sequence 42, Appl |
| 9          | 315   | 100.0       | 293    | 10 US-09-302-863-2    | Sequence 2, Appl  |
| 10         | 315   | 100.0       | 293    | 10 US-09-855-564-2    | Sequence 2, Appl  |
| 11         | 315   | 100.0       | 293    | 13 US-10-087-192-1650 | Sequence 1650, Ap |
| 12         | 315   | 100.0       | 293    | 13 US-10-084-971-2    | Sequence 2, Appl  |
| 13         | 315   | 100.0       | 293    | 14 US-10-068-725-4    | Sequence 4, Appl  |

|    |       |       |      |    |                      |                   |
|----|-------|-------|------|----|----------------------|-------------------|
| 14 | 315   | 100.0 | 293  | 14 | US-10-151-882-46     | Sequence 46, Appl |
| 15 | 315   | 100.0 | 293  | 14 | US-10-293-816-2      | Sequence 2, Appl  |
| 16 | 315   | 100.0 | 293  | 14 | US-10-008-063-8      | Sequence 8, Appl  |
| 17 | 315   | 100.0 | 293  | 14 | US-10-152-363A-2     | Sequence 2, Appl  |
| 18 | 315   | 100.0 | 293  | 14 | US-10-268-951-22     | Sequence 22, Appl |
| 19 | 315   | 100.0 | 293  | 15 | US-10-258-368-1      | Sequence 1, Appl  |
| 20 | 315   | 100.0 | 293  | 15 | US-10-618-797-4      | Sequence 4, Appl  |
| 21 | 315   | 100.0 | 293  | 17 | US-10-742-634-7      | Sequence 7, Appl  |
| 22 | 315   | 100.0 | 293  | 17 | US-10-748-112-27     | Sequence 27, Appl |
| 23 | 315   | 100.0 | 301  | 15 | US-10-258-368-12     | Sequence 12, Appl |
| 24 | 310   | 98.4  | 397  | 9  | US-09-854-864-18     | Sequence 18, Appl |
| 25 | 310   | 98.4  | 397  | 9  | US-09-855-158-18     | Sequence 18, Appl |
| 26 | 300.5 | 95.4  | 291  | 9  | US-09-779-050A-43    | Sequence 43, Appl |
| 27 | 287   | 91.1  | 404  | 15 | US-10-258-368-15     | Sequence 15, Appl |
| 28 | 279.5 | 88.7  | 57   | 9  | US-09-779-050A-47    | Sequence 47, Appl |
| 29 | 260   | 82.5  | 392  | 14 | US-10-152-363A-50    | Sequence 50, Appl |
| 30 | 141.5 | 44.9  | 249  | 13 | US-10-087-192-1647   | Sequence 1647, Ap |
| 31 | 85    | 27.0  | 357  | 14 | US-10-152-363A-56    | Sequence 56, Appl |
| 32 | 68    | 21.6  | 305  | 15 | US-10-424-599-181850 | Sequence 181850,  |
| 33 | 66    | 21.0  | 505  | 16 | US-10-437-963-103271 | Sequence 103271,  |
| 34 | 66    | 21.0  | 554  | 9  | US-09-746-491-41     | Sequence 41, Appl |
| 35 | 65    | 20.6  | 112  | 17 | US-10-425-115-199566 | Sequence 199566,  |
| 36 | 64.5  | 20.5  | 402  | 15 | US-10-425-114-63733  | Sequence 63733, A |
| 37 | 64.5  | 20.5  | 403  | 15 | US-10-425-114-63734  | Sequence 63734, A |
| 38 | 64.5  | 20.5  | 404  | 15 | US-10-425-114-42053  | Sequence 42053, A |
| 39 | 64    | 20.3  | 433  | 16 | US-10-437-963-106971 | Sequence 106971,  |
| 40 | 64    | 20.3  | 448  | 16 | US-10-437-963-107712 | Sequence 107712,  |
| 41 | 64    | 20.3  | 1028 | 15 | US-10-424-599-171115 | Sequence 171115,  |
| 42 | 63.5  | 20.2  | 148  | 16 | US-10-437-963-192537 | Sequence 192537,  |
| 43 | 63    | 20.0  | 109  | 17 | US-10-425-115-222291 | Sequence 222291,  |
| 44 | 63    | 20.0  | 1489 | 15 | US-10-343-710-96     | Sequence 96, Appl |
| 45 | 62.5  | 19.8  | 542  | 17 | US-10-425-115-240726 | Sequence 240726,  |

ALIGNMENTS

RESULT 1

US-09-854-864-15  
; Sequence 15, Application US/09854864  
; Patent No. US20020081296A1  
; GENERAL INFORMATION:  
; APPLICANT: THEILL, LARS EYDE  
; APPLICANT: YU, GANG  
; TITLE OF INVENTION: METHODS AND COMPOSITIONS OF MATTER CONCERNING APRIL/G70, BCMA,  
; TITLE OF INVENTION: BLYS/AGP-3, AND TACI  
; FILE REFERENCE: A-686B  
; CURRENT APPLICATION NUMBER: US/09/854,864  
; CURRENT FILING DATE: 2001-09-11  
; PRIOR APPLICATION NUMBER: US 60/204,039  
; PRIOR FILING DATE: 2000-05-12  
; PRIOR APPLICATION NUMBER: US 60/214,591  
; PRIOR FILING DATE: 2000-06-27  
; NUMBER OF SEQ ID NOS: 31  
; SOFTWARE: PatentIn version 3.1  
; SEQ ID NO 15  
; LENGTH: 166  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-09-854-864-15

Query Match 100.0%; Score 315; DB 9; Length 166;  
Best Local Similarity 100.0%; Pred.No. 1.5e-30;  
Matches 62; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 ENKLRSPVNLPELRQRSGEVNNSDNGRYQGLHGRSEASPALPGLKLSADQVALVY 60  
Db 105 ENKLRSPVNLPELRQRSGEVNNSDNGRYQGLHGRSEASPALPGLKLSADQVALVY 164

QY 61 ST 62

Db 165 ST 166

```
RESULT 2
US-09-855-158-15
; Sequence 15, Application US/09855158
; Publication No. US20020086018A1
; GENERAL INFORMATION:
; APPLICANT: THEILL, LARS EYDE
; APPLICANT: YU, GANG
; TITLE OF INVENTION: METHODS AND COMPOSITIONS OF MATTER CONCERNING APRIL/G70, BCMA, BL
; FILE REFERENCE: A-686A
; CURRENT FILING DATE: 2001-09-11
; PRIOR APPLICATION NUMBER: US 60/214,591
; PRIOR FILING DATE: 2000-06-27
; PRIOR APPLICATION NUMBER: US 60/204,039
; PRIOR FILING DATE: 2000-05-12
; NUMBER OF SEQ ID NOS: 30
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 15
; LENGTH: 166
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-855-158-15

Query Match      100.0%; Score 315; DB 9; Length 166;
Best Local Similarity 100.0%; Pred. No. 1.5e-30;
Matches 62; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ENKLSPVNLPPELRRQSRGSEVNNSDNSGRYQGLEHGRGSEASPALPGLKLSADQVALVY 60
Db 105 ENKLSPVNLPPELRRQSRGSEVNNSDNSGRYQGLEHGRGSEASPALPGLKLSADQVALVY 164

QY 61 ST 62
Db 165 ST 166

RESULT 3
US-10-293-816-6
; Sequence 6, Application US/10293816
; Publication No. US20030082173A1
; GENERAL INFORMATION:
; APPLICANT: Bram, Richard J.
; APPLICANT: Von Bulow, Gotz
; TITLE OF INVENTION: A LYMPHOCYTE SURFACE RECEPTOR THAT BINDS
; FILE REFERENCE: 44158/254623
; CURRENT APPLICATION NUMBER: US/10/293,816
; CURRENT FILING DATE: 2002-11-12
; PRIOR APPLICATION NUMBER: US 09/782,857
; PRIOR FILING DATE: 2001-02-14
; PRIOR APPLICATION NUMBER: US 09/290,333
; PRIOR FILING DATE: 1999-04-12
; PRIOR APPLICATION NUMBER: US 08/810,572
; PRIOR FILING DATE: 1997-03-03
; NUMBER OF SEQ ID NOS: 11
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 6
; LENGTH: 166
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-293-816-6

Query Match      100.0%; Score 315; DB 14; Length 166;
Best Local Similarity 100.0%; Pred. No. 1.5e-30;
Matches 62; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ENKLSPVNLPPELRRQSRGSEVNNSDNSGRYQGLEHGRGSEASPALPGLKLSADQVALVY 60
Db 105 ENKLSPVNLPPELRRQSRGSEVNNSDNSGRYQGLEHGRGSEASPALPGLKLSADQVALVY 164

QY 61 ST 62

RESULT 4
US-09-879-919-22
; Sequence 22, Application US/09879919
; Patent No. US20020064829A1
; GENERAL INFORMATION:
; APPLICANT: YU, GUO-LIANG, et al.
; TITLE OF INVENTION: Human Tumor Necrosis Factor Delta and Epsilon
; FILE REFERENCE: PF253P1
; CURRENT APPLICATION NUMBER: US/09/879,919
; CURRENT FILING DATE: 2001-06-14
; PRIOR APPLICATION NUMBER: 60/293,499
; PRIOR FILING DATE: 2001-05-25
; PRIOR APPLICATION NUMBER: 60/277,978
; PRIOR FILING DATE: 2001-03-23
; PRIOR APPLICATION NUMBER: 60/276,248
; PRIOR FILING DATE: 2001-03-16
; PRIOR APPLICATION NUMBER: 60/254,875
; PRIOR FILING DATE: 2000-12-13
; PRIOR APPLICATION NUMBER: 60/241,952
; PRIOR FILING DATE: 2000-10-23
; PRIOR APPLICATION NUMBER: 60/211,537
; PRIOR FILING DATE: 2000-06-15
; PRIOR APPLICATION NUMBER: 08/815,783
; PRIOR FILING DATE: 1997-03-12
; PRIOR APPLICATION NUMBER: 60/016,812
; PRIOR FILING DATE: 1996-03-14
; NUMBER OF SEQ ID NOS: 26
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 22
; LENGTH: 293
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-879-919-22

Query Match      100.0%; Score 315; DB 9; Length 293;
Best Local Similarity 100.0%; Pred. No. 3.1e-30;
Matches 62; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ENKLSPVNLPPELRRQSRGSEVNNSDNSGRYQGLEHGRGSEASPALPGLKLSADQVALVY 60
Db 105 ENKLSPVNLPPELRRQSRGSEVNNSDNSGRYQGLEHGRGSEASPALPGLKLSADQVALVY 164

QY 61 ST 62
Db 165 ST 166

RESULT 5
US-09-854-864-14
; Sequence 14, Application US/09854864
; Patent No. US20020081296A1
; GENERAL INFORMATION:
; APPLICANT: THEILL, LARS EYDE
; APPLICANT: YU, GANG
; TITLE OF INVENTION: METHODS AND COMPOSITIONS OF MATTER CONCERNING APRIL/G70, BCMA,
; FILE REFERENCE: BLYS/AGP-3, AND TACI
; CURRENT APPLICATION NUMBER: US/09/854,864
; CURRENT FILING DATE: 2001-09-11
; PRIOR APPLICATION NUMBER: US 60/204,039
; PRIOR FILING DATE: 2000-05-12
; PRIOR APPLICATION NUMBER: US 60/214,591
; PRIOR FILING DATE: 2000-06-27
; NUMBER OF SEQ ID NOS: 31
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 14
; LENGTH: 293
; TYPE: PRT
; ORGANISM: Homo sapiens
```

```
US-09-854-864-14
Query Match      100.0%; Score 315; DB 9; Length 293;
Best Local Similarity 100.0%; Pred. No. 3.1e-30;
Matches 62; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ENKLSPVNLPELRRQSRGSEVENNSDNGRYQGLEHGRGSEASPALPGLKLSADQVALVY 60
    |||||
Db 105 ENKLSPVNLPELRRQSRGSEVENNSDNGRYQGLEHGRGSEASPALPGLKLSADQVALVY 164
    ||
QY 61 ST 62
Db 165 ST 166

RESULT 6
US-09-855-158-14
; Sequence 14, Application US/09855158
; Publication No. US20020086018A1
; GENERAL INFORMATION:
; APPLICANT: THEILL, LARS EYDE
; APPLICANT: YU, GANG
; TITLE OF INVENTION: METHODS AND COMPOSITIONS OF MATTER CONCERNING APRIL/G70, BCMA, BL
; TITLE OF INVENTION: 3, AND TACI
; FILE REFERENCE: A-686A
; CURRENT APPLICATION NUMBER: US/09/855,158
; CURRENT FILING DATE: 2001-09-11
; PRIOR APPLICATION NUMBER: US 60/214,591
; PRIOR FILING DATE: 2000-06-27
; PRIOR APPLICATION NUMBER: US 60/204,039
; PRIOR FILING DATE: 2000-05-12
; NUMBER OF SEQ ID NOS: 30
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 14
; LENGTH: 293
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-855-158-14

Query Match      100.0%; Score 315; DB 9; Length 293;
Best Local Similarity 100.0%; Pred. No. 3.1e-30;
Matches 62; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ENKLSPVNLPELRRQSRGSEVENNSDNGRYQGLEHGRGSEASPALPGLKLSADQVALVY 60
    |||||
Db 105 ENKLSPVNLPELRRQSRGSEVENNSDNGRYQGLEHGRGSEASPALPGLKLSADQVALVY 164
    ||
QY 61 ST 62
Db 165 ST 166

RESULT 7
US-09-961-376-2
; Sequence 2, Application US/09961376
; Patent No. US20020106736A1
; GENERAL INFORMATION:
; APPLICANT: Ruben et al.
; TITLE OF INVENTION: Human Tumor Necrosis Factor Receptor TR17
; FILE REFERENCE: PF524FI
; CURRENT APPLICATION NUMBER: US/09/961,376
; CURRENT FILING DATE: 2001-09-25
; PRIOR APPLICATION NUMBER: 60/254,874
; PRIOR FILING DATE: 2000-12-13
; PRIOR APPLICATION NUMBER: 60/235,991
; PRIOR FILING DATE: 2000-09-26
; PRIOR APPLICATION NUMBER: 09/533,822
; PRIOR FILING DATE: 2000-03-24
; PRIOR APPLICATION NUMBER: 60/188,208
; PRIOR FILING DATE: 2000-03-10
; NUMBER OF SEQ ID NOS: 7
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 2

US-09-961-376-2
Query Match      100.0%; Score 315; DB 9; Length 293;
Best Local Similarity 100.0%; Pred. No. 3.1e-30;
Matches 62; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ENKLSPVNLPELRRQSRGSEVENNSDNGRYQGLEHGRGSEASPALPGLKLSADQVALVY 60
    |||||
Db 105 ENKLSPVNLPELRRQSRGSEVENNSDNGRYQGLEHGRGSEASPALPGLKLSADQVALVY 164
    ||
QY 61 ST 62
Db 165 ST 166

RESULT 8
US-09-779-050A-42
; Sequence 42, Application US/09779050A
; Patent No. US20020160416A1
; GENERAL INFORMATION:
; APPLICANT: BOYLE, WILLIAM
; APPLICANT: HSU, HAILING
; TITLE OF INVENTION: RECEPTOR FROM TNF FAMILY
; FILE REFERENCE: A-570B
; CURRENT APPLICATION NUMBER: US/09/779,050A
; CURRENT FILING DATE: 2001-02-12
; PRIOR APPLICATION NUMBER: 60/181,800
; PRIOR FILING DATE: 2000-02-11
; NUMBER OF SEQ ID NOS: 52
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 42
; LENGTH: 293
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-779-050A-42

Query Match      100.0%; Score 315; DB 9; Length 293;
Best Local Similarity 100.0%; Pred. No. 3.1e-30;
Matches 62; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ENKLSPVNLPELRRQSRGSEVENNSDNGRYQGLEHGRGSEASPALPGLKLSADQVALVY 60
    |||||
Db 105 ENKLSPVNLPELRRQSRGSEVENNSDNGRYQGLEHGRGSEASPALPGLKLSADQVALVY 164
    ||
QY 61 ST 62
Db 165 ST 166

RESULT 9
US-09-302-863-2
; Sequence 2, Application US/09302863
; Publication No. US2003002233A1
; GENERAL INFORMATION:
; APPLICANT: Goodwin, Raymond G
; APPLICANT: Din, Wanwan S.
; TITLE OF INVENTION: METHODS OF USE OF THE TACI/TACI-L INTERACTION
; FILE REFERENCE: 2519
; CURRENT APPLICATION NUMBER: US/09/302,863
; CURRENT FILING DATE: 1999-04-30
; NUMBER OF SEQ ID NOS: 5
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 2
; LENGTH: 293
; TYPE: PRT
; ORGANISM: Human
US-09-302-863-2

Query Match      100.0%; Score 315; DB 10; Length 293;
Best Local Similarity 100.0%; Pred. No. 3.1e-30;
```

Matches 62; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 ENKLRSPVNLPPELRRQSRGSEVENNSDNGRYQGLEHGRSEASPALPGLKLSADQVALVY 60  
DB 105 ENKLRSPVNLPPELRRQSRGSEVENNSDNGRYQGLEHGRSEASPALPGLKLSADQVALVY 164  
QY 61 ST 62  
DB 165 ST 166

RESULT 10  
US-09-855-564-2  
; Sequence 2, Application US/09855564  
; Publication No. US20030165986A1  
; GENERAL INFORMATION:  
; APPLICANT: Goodwin, Raymond G  
; TITLE OF INVENTION: METHODS OF USE OF THE TACI/TACI-L INTERACTION  
; FILE REFERENCE: 2519  
; CURRENT APPLICATION NUMBER: US/09/855,564  
; PRIOR FILING DATE: 2001-05-14  
; PRIOR APPLICATION NUMBER: 09/302,863  
; PRIOR FILING DATE: 1999-04-30  
; NUMBER OF SEQ ID NOS: 5  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 2  
; LENGTH: 293  
; TYPE: PRT  
; ORGANISM: Human  
US-09-855-564-2

Query Match 100.0%; Score 315; DB 10; Length 293;  
Best Local Similarity 100.0%; Pred. No. 3.1e-30;  
Matches 62; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 ENKLRSPVNLPPELRRQSRGSEVENNSDNGRYQGLEHGRSEASPALPGLKLSADQVALVY 60  
DB 105 ENKLRSPVNLPPELRRQSRGSEVENNSDNGRYQGLEHGRSEASPALPGLKLSADQVALVY 164  
QY 61 ST 62  
DB 165 ST 166

RESULT 11  
US-10-087-192-1650  
; Sequence 1650, Application US/10087192  
; Publication No. US20020182586A1  
; GENERAL INFORMATION:  
; APPLICANT: Morris, David W.  
; APPLICANT: Engelhard, Eric K.  
; TITLE OF INVENTION: NOVEL COMPOSITIONS AND METHODS FOR  
; FILE REFERENCE: 529452000122  
; CURRENT APPLICATION NUMBER: US/10/087,192  
; CURRENT FILING DATE: 2002-03-01  
; PRIOR APPLICATION NUMBER: US 09/747,377  
; PRIOR FILING DATE: 2000-12-22  
; PRIOR APPLICATION NUMBER: US 09/798,586  
; PRIOR FILING DATE: 2001-03-02  
; NUMBER OF SEQ ID NOS: 2059  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 1650  
; LENGTH: 293  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-10-087-192-1650

Query Match 100.0%; Score 315; DB 13; Length 293;  
Best Local Similarity 100.0%; Pred. No. 3.1e-30;  
Matches 62; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ENKLRSPVNLPPELRRQSRGSEVENNSDNGRYQGLEHGRSEASPALPGLKLSADQVALVY 60  
DB 105 ENKLRSPVNLPPELRRQSRGSEVENNSDNGRYQGLEHGRSEASPALPGLKLSADQVALVY 164  
QY 61 ST 62  
DB 165 ST 166

RESULT 12  
US-10-084-971-2  
; Sequence 2, Application US/10084971  
; Publication No. US20020187526A1  
; GENERAL INFORMATION:  
; APPLICANT: Human Genome Sciences, Inc.  
; TITLE OF INVENTION: Neurokine-alpha Binding Proteins and Methods Based Thereon  
; FILE REFERENCE: PF524PCT  
; CURRENT APPLICATION NUMBER: US/10/084,971  
; CURRENT FILING DATE: 2002-03-01  
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: US/09/533,822  
; PRIOR FILING DATE: EARLIER FILING DATE: 2000-03-24  
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 60/126,599  
; PRIOR FILING DATE: EARLIER FILING DATE: 1999-03-26  
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 60/188,208  
; PRIOR FILING DATE: EARLIER FILING DATE: 1999-03-10  
; NUMBER OF SEQ ID NOS: 5  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 2  
; LENGTH: 293  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-10-084-971-2

Query Match 100.0%; Score 315; DB 13; Length 293;  
Best Local Similarity 100.0%; Pred. No. 3.1e-30;  
Matches 62; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 ENKLRSPVNLPPELRRQSRGSEVENNSDNGRYQGLEHGRSEASPALPGLKLSADQVALVY 60  
DB 105 ENKLRSPVNLPPELRRQSRGSEVENNSDNGRYQGLEHGRSEASPALPGLKLSADQVALVY 164  
QY 61 ST 62  
DB 165 ST 166

RESULT 13  
US-10-068-725-4  
; Sequence 4, Application US/10068725  
; Publication No. US20030012783A1  
; GENERAL INFORMATION:  
; APPLICANT: Kindsvogel, Wayne  
; TITLE OF INVENTION: Antibodies That Bind Both BCMA and TACI  
; FILE REFERENCE: 01-04  
; CURRENT APPLICATION NUMBER: US/10/068,725  
; CURRENT FILING DATE: 2002-02-06  
; PRIOR APPLICATION NUMBER: 60/270,274  
; PRIOR FILING DATE: 2001-02-20  
; PRIOR APPLICATION NUMBER: 60/283,447  
; PRIOR FILING DATE: 2001-04-12  
; NUMBER OF SEQ ID NOS: 5  
; SOFTWARE: FastSeq for Windows Version 3.0  
; SEQ ID NO 4  
; LENGTH: 293  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-10-068-725-4

Query Match 100.0%; Score 315; DB 14; Length 293;  
Best Local Similarity 100.0%; Pred. No. 3.1e-30;  
Matches 62; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 ENKLRSPVNLPPELRRQSRGSEVENNSDNGRYQGLEHGRSEASPALPGLKLSADQVALVY 60

Db 105 ENKLRSPVNLPELRRQSRGEVNNSDNSGRYQGLEHGRSEASPALPGLKLSADQVALVY 164  
Qy 61 ST 62  
Db 165 ST 166

RESULT 14  
US-10-151-882-46  
; Sequence 46, Application US/10151882  
; Publication No. US20030059862A1  
; GENERAL INFORMATION:  
; APPLICANT: Ruben, Steven M.  
; TITLE OF INVENTION: Antibodies Against Tumor Necrosis Factor Delta (APRIL)  
; FILE REFERENCE: PF554  
; CURRENT APPLICATION NUMBER: US/10/151,882  
; CURRENT FILING DATE: 2002-05-22  
; PRIOR APPLICATION NUMBER: 60/293,100  
; PRIOR FILING DATE: 2001-05-24  
; NUMBER OF SEQ ID NOS: 48  
; SOFTWARE: PatentIn version 3.0  
; SEQ ID NO 46  
; LENGTH: 293  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-10-151-882-46

Query Match 100.0%; Score 315; DB 14; Length 293;  
Best Local Similarity 100.0%; Pred. No. 3.1e-30;  
Matches 62; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
Qy 1 ENKLRSPVNLPELRRQSRGEVNNSDNSGRYQGLEHGRSEASPALPGLKLSADQVALVY 60  
Db 105 ENKLRSPVNLPELRRQSRGEVNNSDNSGRYQGLEHGRSEASPALPGLKLSADQVALVY 164  
Qy 61 ST 62  
Db 165 ST 166

RESULT 15  
US-10-293-816-2  
; Sequence 2, Application US/10293816  
; Publication No. US20030082173A1  
; GENERAL INFORMATION:  
; APPLICANT: Bram, Richard J.  
; APPLICANT: Von Bulow, Goetz  
; TITLE OF INVENTION: A LYMPHOCYTE SURFACE RECEPTOR THAT BINDS  
; TITLE OF INVENTION: CAML AND METHODS OF USE THEREOF  
; FILE REFERENCE: 44158/254623  
; CURRENT APPLICATION NUMBER: US/10/293,816  
; CURRENT FILING DATE: 2002-11-12  
; PRIOR APPLICATION NUMBER: US 09/782,857  
; PRIOR FILING DATE: 2001-02-14  
; PRIOR APPLICATION NUMBER: US 09/290,333  
; PRIOR FILING DATE: 1999-04-12  
; PRIOR APPLICATION NUMBER: US 08/810,572  
; PRIOR FILING DATE: 1997-03-03  
; NUMBER OF SEQ ID NOS: 11  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 2  
; LENGTH: 293  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-10-293-816-2

Query Match 100.0%; Score 315; DB 14; Length 293;  
Best Local Similarity 100.0%; Pred. No. 3.1e-30;  
Matches 62; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
Qy 1 ENKLRSPVNLPELRRQSRGEVNNSDNSGRYQGLEHGRSEASPALPGLKLSADQVALVY 60

Db 105 ENKLRSPVNLPELRRQSRGEVNNSDNSGRYQGLEHGRSEASPALPGLKLSADQVALVY 164  
Qy 61 ST 62  
Db 165 ST 166  
Search completed: November 20, 2004, 00:00:28  
Job time : 172.535 secs

**This Page Blank (uspto)**



GenCore version 5.1.6  
Copyright (c) 1993 - 2004 Compugen Ltd.

OM protein - protein search, using sw model

Run on: November 19, 2004, 23:34:49 ; Search time 22.7042 Seconds  
(without alignments)  
262.746 Million cell updates/sec

Title: US-10-068-725-4\_COPY\_105\_166

Perfect score: 315  
Sequence: 1 ENKLRSPVNLPPELRRQSG.....SPALPGLKLSADQVALVYST 62

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : PIR 79:\*  
1: pir1:\*  
2: pir2:\*  
3: pir3:\*  
4: pir4:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Score | Query Match | Length | ID     | Description        |
|------------|-------|-------------|--------|--------|--------------------|
| 1          | 62.5  | 19.8        | 1741   | T13610 | parallel sister ch |
| 2          | 62.5  | 19.8        | 1768   | T13349 | parallel sister ch |
| 3          | 62    | 19.7        | 806    | S22765 | heterogeneous ribo |
| 4          | 61.5  | 19.5        | 250    | T23644 | hypothetical prote |
| 5          | 61.5  | 19.5        | 470    | AH3594 | virulence protein  |
| 6          | 61    | 19.4        | 1028   | A56038 | DNA-binding protei |
| 7          | 61    | 19.4        | 1213   | S16356 | ovo protein - frui |
| 8          | 60.5  | 19.2        | 379    | T29518 | hypothetical prote |
| 9          | 60.5  | 19.2        | 713    | B84583 | hypothetical prote |
| 10         | 60    | 19.0        | 717    | T22938 | hypothetical prote |
| 11         | 59    | 18.7        | 307    | T40615 | transcription init |
| 12         | 59    | 18.7        | 430    | A46216 | transcription fact |
| 13         | 59    | 18.7        | 512    | JC4164 | catalase [EC 1.11. |
| 14         | 59    | 18.7        | 532    | T42369 | catalase [EC 1.11. |
| 15         | 59    | 18.7        | 565    | T10696 | legumin-like prote |
| 16         | 59    | 18.7        | 626    | T09345 | hypothetical prote |
| 17         | 59    | 18.7        | 2342   | T13412 | hypothetical prote |
| 18         | 58.5  | 18.6        | 246    | T12585 | Dc3 promoter-bindi |
| 19         | 58.5  | 18.6        | 365    | T43286 | cet-1 protein - Ca |
| 20         | 58.5  | 18.6        | 458    | S24457 | hypothetical prote |
| 21         | 58.5  | 18.6        | 535    | S74703 | hypothetical prote |
| 22         | 58.5  | 18.6        | 750    | D88082 | protein T05A8.4 [i |
| 23         | 58.5  | 18.6        | 769    | T16245 | hypothetical prote |
| 24         | 58    | 18.4        | 255    | T44991 | oxidoreductase [m  |
| 25         | 58    | 18.4        | 351    | B89781 | conserved hypothet |
| 26         | 58    | 18.4        | 504    | T10698 | legumin-like prote |
| 27         | 58    | 18.4        | 508    | B81594 | hypothetical prote |
| 28         | 58    | 18.4        | 508    | E86549 | hypothetical prote |
| 29         | 58    | 18.4        | 508    | C72074 | hypothetical prote |

|    |      |      |      |   |        |                    |
|----|------|------|------|---|--------|--------------------|
| 30 | 58   | 18.4 | 583  | 2 | S43139 | phytoene dehydroge |
| 31 | 58   | 18.4 | 621  | 2 | I38880 | eleven-nineteen ly |
| 32 | 58   | 18.4 | 900  | 2 | S46101 | hypothetical prote |
| 33 | 58   | 18.4 | 1615 | 2 | B49502 | protein-tyrosine-p |
| 34 | 58   | 18.4 | 1767 | 2 | A49502 | protein-tyrosine-p |
| 35 | 57.5 | 18.3 | 173  | 2 | T51868 | hypothetical prote |
| 36 | 57.5 | 18.3 | 404  | 2 | A82188 | hypothetical prote |
| 37 | 57.5 | 18.3 | 414  | 2 | C75461 | hypothetical prote |
| 38 | 57   | 18.1 | 349  | 2 | S57538 | END3 protein - yea |
| 39 | 57   | 18.1 | 377  | 1 | B0AG58 | virB10 protein - A |
| 40 | 57   | 18.1 | 377  | 2 | A83249 | component of type  |
| 41 | 56.5 | 17.9 | 465  | 2 | AH2092 | hypothetical prote |
| 42 | 56.5 | 17.9 | 837  | 2 | S54624 | KOD1 protein - yea |
| 43 | 56   | 17.8 | 143  | 2 | H72610 | hypothetical prote |
| 44 | 56   | 17.8 | 176  | 2 | A86159 | hypothetical prote |
| 45 | 56   | 17.8 | 427  | 2 | S38032 | hypothetical prote |

ALIGNMENTS

RESULT 1

T13610  
Parallel sister chromatids protein - fruit fly (Drosophila melanogaster)  
C:Species: Drosophila melanogaster  
C>Date: 13-Aug-1999 #sequence\_revision 13-Aug-1999 #text\_change 09-Jul-2004  
C:Accession: T13610  
R:Murphy, L.; Harris, D.; Barrell, B.  
submitted to the EMBL Data Library, April 1999  
A:Description: Sequencing the distal X chromosome of Drosophila melanogaster.  
A:Reference number: Z17668  
A:Accession: T13610  
A:Status: preliminary; translated from GB/EMBL/DBDJ  
A:Molecule type: DNA  
A:Residues: 1-1741 <MUR>  
A:Cross-references: UNIPROT:O46095; EMBL:Z98269; NID:e1355202; PID:e1251076; PIDN:CAB109  
C:Genetics:  
A:Cross-references: FlyBase:FBgn0013432  
A:Introns: 348/3; 1219/3; 1500/3; 1557/2; 1587/1; 1650/3  
A>Note: EG:87B1.2

Query Match

Best Local Similarity 19.8%; Score 62.5; DB 2; Length 1741;  
Matches 17; Conservative 8; Mismatches 15; Indels 13; Gaps 2;

QY 1 ENKLRSPVNLPPELRRQRS-----GEVENNSDNGRYQGLHRGSEASP 44

Db 870 EEEQTPAKIPHTDREHSPDHPDPPDDELNNNSNS-----SLQHDGSSSP 918

RESULT 2

T13349  
Parallel sister chromatids protein - fruit fly (Drosophila melanogaster)  
C:Species: Drosophila melanogaster  
C>Date: 13-Aug-1999 #sequence\_revision 13-Aug-1999 #text\_change 09-Jul-2004  
C:Accession: T13349  
R:Gandhi, R.L.; Goldberg, M.L.  
submitted to the EMBL Data Library, November 1995  
A:Reference number: Z17657  
A:Accession: T13349  
A:Status: preliminary; translated from GB/EMBL/DBDJ  
A:Molecule type: mRNA  
A:Residues: 1-1768 <GAN>  
A:Cross-references: UNIPROT:Q24153; EMBL:U40214; NID:g1100982; PID:g1100983; PIDN:AAA912

Query Match 19.8%; Score 62.5; DB 2; Length 1768;

Best Local Similarity 32.1%; Pred. No. 58;  
Matches 17; Conservative 8; Mismatches 15; Indels 13; Gaps 2;

QY 1 ENKLRSPVNLPPELRRQRS-----GEVENNSDNGRYQGLHRGSEASP 44

|                       |              |                |                |             |
|-----------------------|--------------|----------------|----------------|-------------|
| Query Match           | 19.5%;       | Score 61.5;    | DB 2;          | Length 250; |
| Best Local Similarity | 36.7%;       | Pred. NO. 8.3; |                |             |
| Matches 18;           | Conservative | 4;             | Mismatches 26; | Indels 1;   |
|                       |              |                |                | Gaps 1;     |

C;Spec:

Query Match 19.5%; Score 61.5; DB 2; Length 250;  
Best Local Similarity 36.7%; Pred. No. 8.3;  
Matches 18; Conservative 4; Mismatches 26; Indels

C/Accession: S16356  
R;Mevel-Ninio, M.; Terracol, R.; Kafatos, F.C.  
EMBO J. 10, 2259-2266, 1991  
A/Title: The ovo gene of *Drosophila* encodes a zinc finger protein required for female sex  
A/Reference number: S16356; MUID:91293102; PMID:1712294  
A/Accession: S16356  
A/Status: preliminary  
A/Molecule type: DNA  
A/Residues: 1-1213 <MEV>  
A/Cross-references: UNIPROT:Q8T8L9; EMBL:X59772  
C/Genetics:  
A/Gene: FlyBase:ovo  
A/Cross-references: FlyBase:FBgn0003028  
A/Introns: 931/3; 1152/3

Best Local Similarity 36.1%; Pred. No. 57;  
Matches 13; Conservative 6; Mismatches 17; Indels 0; Gaps 0;

Db 384 LPFFYSLKSGQOSTASNTGTQSPGASHFNANPA 419

T29518  
hypothetical protein T25F10.2 - *Caenorhabditis elegans*  
C/Species: *Caenorhabditis elegans*  
C/Date: 15-Oct-1999 #sequence\_revision 15-Oct-1999 #text\_change 09-Jul-2004  
C/Accession: T29518

**A;Description:** The sequence of *C. elegans* cosmid T25F10.

A;Accession: T29518

A/Molecule type: DNA  
A:Residues: 1-379 <PAU>

A; Experimental source: S

**A;Gene: CESP:T25F10.2**

A; Introns: 96/3; 129/3; 153/3; 250/3; 286/1; 324/3; 362/2

Query Match

Best Local Similarity 34.1%; Pred. No. 18;

1  
2  
3  
4  
5  
6  
7  
8  
9  
10  
11  
12  
13  
14  
15  
16  
17  
18  
19  
20  
21  
22  
23  
24  
25  
26  
27  
28  
29  
30  
31  
32  
33  
34  
35  
36  
37  
38  
39  
40  
41  
42  
43  
44  
45  
46  
47  
48  
49  
50  
51  
52  
53  
54  
55  
56  
57  
58  
59  
60  
61  
62  
63  
64  
65  
66  
67  
68  
69  
70  
71  
72  
73  
74  
75  
76  
77  
78  
79  
80  
81  
82  
83  
84  
85  
86  
87  
88  
89  
90  
91  
92  
93  
94  
95  
96  
97  
98  
99  
100  
101  
102  
103  
104  
105  
106  
107  
108  
109  
110  
111  
112  
113  
114  
115  
116  
117  
118  
119  
120  
121  
122  
123  
124  
125  
126  
127  
128  
129  
130  
131  
132  
133  
134  
135  
136  
137  
138  
139  
140  
141  
142  
143  
144  
145  
146  
147  
148  
149  
150  
151  
152  
153  
154  
155  
156  
157  
158  
159  
160  
161  
162  
163  
164  
165  
166  
167  
168  
169  
170  
171  
172  
173  
174  
175  
176  
177  
178  
179  
180  
181  
182  
183  
184  
185  
186  
187  
188  
189  
190  
191  
192  
193  
194  
195  
196  
197  
198  
199  
200  
201  
202  
203  
204  
205  
206  
207  
208  
209  
210  
211  
212  
213  
214  
215  
216  
217  
218  
219  
220  
221  
222  
223  
224  
225  
226  
227  
228  
229  
230  
231  
232  
233  
234  
235  
236  
237  
238  
239  
240  
241  
242  
243  
244  
245  
246  
247  
248  
249  
250  
251  
252  
253  
254  
255  
256  
257  
258  
259  
260  
261  
262  
263  
264  
265  
266  
267  
268  
269  
270  
271  
272  
273  
274  
275  
276  
277  
278  
279  
280  
281  
282  
283  
284  
285  
286  
287  
288  
289  
290  
291  
292  
293  
294  
295  
296  
297  
298  
299  
300  
301  
302  
303  
304  
305  
306  
307  
308  
309  
310  
311  
312  
313  
314  
315  
316  
317  
318  
319  
320  
321  
322  
323  
324  
325  
326  
327  
328  
329  
330  
331  
332  
333  
334  
335  
336  
337  
338  
339  
340  
341  
342  
343  
344  
345  
346  
347  
348  
349  
350  
351  
352  
353  
354  
355  
356  
357  
358  
359  
360  
361  
362  
363  
364  
365  
366  
367  
368  
369  
370  
371  
372  
373  
374  
375  
376  
377  
378  
379  
380  
381  
382  
383  
384  
385  
386  
387  
388  
389  
390  
391  
392  
393  
394  
395  
396  
397  
398  
399  
400  
401  
402  
403  
404  
405  
406  
407  
408  
409  
410  
411  
412  
413  
414  
415  
416  
417  
418  
419  
420  
421  
422  
423  
424  
425  
426  
427  
428  
429  
430  
431  
432  
433  
434  
435  
436  
437  
438  
439  
440  
441  
442  
443  
444  
445  
446  
447  
448  
449  
450  
451  
452  
453  
454  
455  
456  
457  
458  
459  
460  
461  
462  
463  
464  
465  
466  
467  
468  
469  
470  
471  
472  
473  
474  
475  
476  
477  
478  
479  
480  
481  
482  
483  
484  
485  
486  
487  
488  
489  
490  
491  
492  
493  
494  
495  
496  
497  
498  
499  
500  
501  
502  
503  
504  
505  
506  
507  
508  
509  
510  
511  
512  
513  
514  
515  
516  
517  
518  
519  
520  
521  
522  
523  
524  
525  
526  
527  
528  
529  
530  
531  
532  
533  
534  
535  
536  
537  
538  
539  
540  
541  
542  
543  
544  
545  
546  
547  
548  
549  
550  
551  
552  
553  
554  
555  
556  
557  
558  
559  
560  
561  
562  
563  
564  
565  
566  
567  
568  
569  
570  
571  
572  
573  
574  
575  
576  
577  
578  
579  
580  
581  
582  
583  
584  
585  
586  
587  
588  
589  
590  
591  
592  
593  
594  
595  
596  
597  
598  
599  
600  
601  
602  
603  
604  
605  
606  
607  
608  
609  
610  
611  
612  
613  
614  
615  
616  
617  
618  
619  
620  
621  
622  
623  
624  
625  
626  
627  
628  
629  
630  
631  
632  
633  
634  
635  
636  
637  
638  
639  
640  
641  
642  
643  
644  
645  
646  
647  
648  
649  
650  
651  
652  
653  
654  
655  
656  
657  
658  
659  
660  
661  
662  
663  
664  
665  
666  
667  
668  
669  
670  
671  
672  
673  
674  
675  
676  
677  
678  
679  
680  
681  
682  
683  
684  
685  
686  
687  
688  
689  
690  
691  
692  
693  
694  
695  
696  
697  
698  
699  
700  
701  
702  
703  
704  
705  
706  
707  
708  
709  
710  
711  
712  
713  
714  
715  
716  
717  
718  
719  
720  
721  
722  
723  
724  
725  
726  
727  
728  
729  
730  
731  
732  
733  
734  
735  
736  
737  
738  
739  
740  
741  
742  
743  
744  
745  
746  
747  
748  
749  
750  
751  
752  
753  
754  
755  
756  
757  
758  
759  
760  
761  
762  
763  
764  
765  
766  
767  
768  
769  
770  
771  
772  
773  
774  
775  
776  
777  
778  
779  
780  
781  
782  
783  
784  
785  
786  
787  
788  
789  
790  
791  
792  
793  
794  
795  
796  
797  
798  
799  
800  
801  
802  
803  
804  
805  
806  
807  
808  
809  
810  
811  
812  
813  
814  
815  
816  
817  
818  
819  
820  
821  
822  
823  
824  
825  
826  
827  
828  
829  
830  
831  
832  
833  
834  
835  
836  
837  
838  
839  
840  
84

224 SNISEPSSITBPKPSLOT-CNEEPKIBKVCBVLATPEBENT

B84583

C;Species: Arabidopsis thaliana (mouse-ear cress)

C;Accession: B84383  
R:Lin. X.; Kaul. S.: Roum[ev. S. D.: Shea. T. P.: Benito. M. T.: Town. C. D.:

euss, D.; Nierman, W.C.; White, O.; Eisen, J.A.; Salzberg, S.L.; Fraser, C.M.; Venter, J. Nature 402, 761-768, 1999

A;Reference number: A84420; MUID:20083487; PMID:10617197

A;Status: preliminary

A; references: I-13 &  
A: Cross-references:



Search completed: November 19, 2004, 23:44:53  
Job time : 24.7042 secs

***This Page Blank (uspto)***

GenCore version 5.1.1.6  
Copyright (c) 1993 - 2004 Compugen Ltd.

OM protein - protein search, using sw model

Run on: November 19, 2004, 23:32:13 ; Search time 221.803 Seconds  
(without alignments)  
160.833 Million cell updates/sec

Title: US-10-068-725-4\_COPY\_105\_166

Perfect score: 315

Sequence: 1 ENKLRSPVNLPELRQRSG.....SPALPGLKLSADQVALVYST 62

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1825181 seqs, 575374646 residues

Total number of hits satisfying chosen parameters: 1825181

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : UniProt 02.\*

1: uniprot\_sprot.\*

2: uniprot\_tr embl.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Score | Query Match | Length | ID         | Description         |
|------------|-------|-------------|--------|------------|---------------------|
| 1          | 315   | 100.0       | 247    | Q726F5     | Q726F5 homo sapien  |
| 2          | 315   | 100.0       | 293    | T13X_HUMAN | O14836 homo sapien  |
| 3          | 141.5 | 44.9        | 249    | T13X_MOUSE | Q9et35 mus musculus |
| 4          | 140   | 44.4        | 156    | Q9N146     | Q9n146 macaca mula  |
| 5          | 84.5  | 26.8        | 702    | Q9VH96     | Q9vh96 drosophila   |
| 6          | 66    | 21.0        | 480    | Q7YI18     | Q7yI18 strongyloce  |
| 7          | 66    | 21.0        | 480    | Q9GUY6     | Q9guy6 hemientrot   |
| 8          | 66    | 21.0        | 497    | Q942X2     | Q942x2 oryza sativ  |
| 9          | 66    | 21.0        | 509    | Q98KE4     | Q98ke4 rhizobium l  |
| 10         | 66    | 21.0        | 546    | Q7VBZ9     | Q7vBz9 prochloroco  |
| 11         | 66    | 21.0        | 554    | Q9JHT9     | Q9jht9 mus musculus |
| 12         | 66    | 21.0        | 620    | Q923H2     | Q923h2 mus musculus |
| 13         | 66    | 21.0        | 710    | Q8CHT1     | Q8cht1 mus musculus |
| 14         | 65.5  | 20.8        | 677    | Q8TEJ7     | Q8tej7 homo sapien  |
| 15         | 65    | 20.6        | 835    | Q8KRE4     | Q8kre4 agrobacteri  |
| 16         | 64.5  | 20.5        | 87     | Q8AY96     | Q8ay96 ictalurus p  |
| 17         | 64.5  | 20.5        | 358    | Q96BE7     | Q96be7 homo sapien  |
| 18         | 64    | 20.3        | 433    | Q7XK69     | Q7xk69 oryza sativ  |
| 19         | 63.5  | 20.2        | 800    | Q6BJB7     | Q6bjb7 debaryomyce  |
| 20         | 63.5  | 20.2        | 1665   | Q6FIZ5     | Q6fiz5 candida gla  |
| 21         | 63    | 20.0        | 3374   | Q8UJZ3     | Q8ujz3 montana myo  |
| 22         | 62.5  | 19.8        | 315    | Q73U36     | Q73u36 mycobacteri  |
| 23         | 62.5  | 19.8        | 315    | AA506082   | AA506082 mycobacte  |
| 24         | 62.5  | 19.8        | 1092   | Q7KVZ8     | Q7kvz8 drosophila   |
| 25         | 62.5  | 19.8        | 1092   | AAF45735   | AAF45735 drosophil  |
| 26         | 62.5  | 19.8        | 1108   | Q8MR12     | Q8mr12 drosophila   |
| 27         | 62.5  | 19.8        | 1741   | O46095     | O46095 drosophila   |
| 28         | 62.5  | 19.8        | 1741   | Q9W517     | Q9w517 drosophila   |
| 29         | 62.5  | 19.8        | 1768   | Q24153     | Q24153 drosophila   |
| 30         | 62.5  | 19.8        | 6858   | Q7QWU1     | Q7qwU1 giardia lam  |
| 31         | 62    | 19.7        | 824    | ROU_HUMAN  | Q00839 homo sapien  |

RESULT 1

Q726F5

ID Q726F5 PRELIMINARY; PRT; 247 AA.

AC Q726F5; DT 01-OCT-2003 (TrEMBLrel. 25, Created)

DT 01-OCT-2003 (TrEMBLrel. 25, Last sequence update)

DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)

DE Transmembrane activator and CAML interactor.

GN Name=TNFRSF13B;

OS Homo sapiens (Human)

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

OC NCBI\_TaxID=9606;

RN [1] SEQUENCE FROM N.A.

RA Zhou G., Ke R., Li H., Zheng G., Shen C., Lin L., Yang S.;

RL Submitted (MAY-2003) to the EMBL/GenBank/DBJ databases.

DR EMBL; AY302137; AAP57629.1; -

DR GO; GO:0016021; C:integral to membrane; IEA.

KW Transmembrane.

SQ SEQUENCE 247 AA; 26664 MW; 850E1F4C2578E8E6 CRC64;

Query Match 100.0%; Score 315; DB 2; Length 247;

Best Local Similarity 100.0%; Pred. No. 7.7e-29;

Matches 62; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ENKLRSPVNLPELRQRSGEVNNSGRYQGLEHGRSEASPALPGLKLSADQVALVY 60

Db 59 ENKLRSPVNLPELRQRSGEVNNSGRYQGLEHGRSEASPALPGLKLSADQVALVY 118

QY 61 ST 62

Db 119 ST 120

RESULT 2

T13X\_HUMAN

ID T13X\_HUMAN STANDARD; PRT; 293 AA.

AC O14836; DT 28-FEB-2003 (Rel. 41, Created)

DT 28-FEB-2003 (Rel. 41, Last sequence update)

DT 05-JUL-2004 (Rel. 44, Last annotation update)

DE Tumor necrosis factor receptor superfamily member 13B (Transmembrane

DE activator and CAML interactor).

GN Name=TNFRSF13B; Synonyms=TACI;

OC Homo sapiens (Human)

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

OC NCBI\_TaxID=9606;

RN [1] SEQUENCE FROM N.A.

RP TISSUE=B-cell;

RC MEDLINE=97458245; PubMed=9311921;

RA von Buelow G.-U., Bram R.J.;

RT "NF-AT activation induced by a CAML-interacting member of the tumor  
 RT necrosis factor receptor superfamily";  
 RL Science 278:138-141(1997).  
 RN [2]  
 RP  
 RC TISSUE=Blood;  
 RX MEDLINE=22389257; PubMed=12477932; DOI=10.1073/pnas.242603899;  
 RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,  
 RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,  
 RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,  
 RA Hopkins R.F., Jordan H., Moore T.I., Max S.I., Wang J., Hsieh F.,  
 RA Datchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,  
 RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,  
 RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,  
 RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullany S.J.,  
 RA Bobak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,  
 RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,  
 RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,  
 RA Fahey J., Helton E., Kettman M., Madan A., Rodriguez S., Sanchez A.,  
 RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,  
 RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,  
 RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,  
 RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smallos D.E.,  
 RA Schnerch A., Schein J.B., Jones S.J.M., Matra M.A.;  
 RA "Generation and initial analysis of more than 15,000 full-length human  
 RT and mouse cDNA sequences";  
 RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).  
 RN [3]  
 RP FUNCTION.  
 RX MEDLINE=20519647; PubMed=10956646; DOI=10.1074/jbc.M005224200;  
 RA Wu Y., Bressette D., Carrell J.A., Kaufman T., Peng P., Taylor K.,  
 RA Gan Y., Cho Y.H., Garcia A.D., Gollatz E., Dimke D., Lapleur D.,  
 RA Migone T.S., Nardelli B., Wei P., Ruben S.M., Ullrich S.J.,  
 RA Olsen H.S., Kanakara P., Moore P.A., Baker K.P.;  
 RA "Tumor necrosis factor (TNF) receptor superfamily member TACI is a  
 RT high affinity receptor for TNF family members APRIL and BlyS";  
 RL J. Biol. Chem. 275:35478-35485(2000).  
 RN [4]  
 RP FUNCTION.  
 RX MEDLINE=21170294; PubMed=10973284; DOI=10.1038/79802;  
 RA Yu G., Boone T., Delaney J., Hawkins N., Kelley M., Ramakrishnan M.,  
 RA McCabe S., Qiu W.R., Kornuc M., Xia X.-Z., Guo J., Stolina M.,  
 RA Boyle W.J., Sarosi I., Hsu H., Senaldi G., Theill L.E.;  
 RA "APRIL and TALL-1 and receptors BCMA and TACI: system for regulating  
 RT humoral immunity";  
 RL Nat. Immunol. 1:252-256(2000).  
 RN [5]  
 RP INTERACTIONS WITH TRAF2 AND TRAF5.  
 RX MEDLINE=20341628; PubMed=10880535;  
 RA Xia X.-Z., Treanor J., Senaldi G., Khare S.D., Boone T., Kelley M.,  
 RA Theill L.E., Colombero A., Solovjev I., Lee F., McCabe S., Elliott R.,  
 RA Miner K., Hawkins N., Guo J., Stolina M., Yu G., Wang J., Delaney J.,  
 RA Meng S.Y., Boyle W.J., Hsu H.;  
 RA "TACI is a TRAF-interacting receptor for TALL-1, a tumor necrosis  
 RT factor family member involved in B cell regulation";  
 RL J. Exp. Med. 192:137-143(2000).  
 CC -1- FUNCTION: Receptor for TNFSF13/APRIL and TNFSF13B/TALL1/BAFF/BLYS  
 CC that binds both ligands with similar high affinity. Mediates  
 CC calcineurin-dependent activation of NF-AT, as well as activation  
 CC of NF-kappa-B and AP-1. Involved in the stimulation of B- and T-  
 CC cell function and the regulation of humoral immunity.  
 CC -1- SUBUNIT: Binds TRAF2, TRAF5 and TRAF6. Binds the NH2-terminal  
 CC domain of CAML with its C-terminus.  
 CC -1- SUBCELLULAR LOCATION: Type III membrane protein.  
 CC -1- TISSUE SPECIFICITY: Highly expressed in spleen, thymus, small  
 CC intestine and peripheral blood leukocytes. Expressed in resting B-  
 CC cells and activated T-cells, but not in resting T-cells.  
 CC -1- SIMILARITY: Contains 2 TNFR-Cys repeats.  
 CC -1- CAUTION: It is uncertain whether Met-1 or Met-31 is the initiator.  
 CC This SWISS-PROT entry is copyright. It is produced through a collaboration  
 CC between the Swiss Institute of Bioinformatics and the EMBL outstation -  
 CC the European Bioinformatics Institute. There are no restrictions on its

CC use by non-profit institutions as long as its content is in no way  
 CC modified and this statement is not removed. Usage by and for commercial  
 CC entities requires a license agreement (see <http://www.isb-sib.ch/announce/>  
 CC or send an email to [license@isb-sib.ch](mailto:license@isb-sib.ch)).  
 CC -----  
 CC EMBL; AF023614; AAC51790.1; --  
 CC EMBL; BC028072; AAH28072.1; --  
 CC HSSP; Q9Y275; IQOD. --  
 CC GENE; HGNC:18153; TNFRSF13B.  
 CC MIM; 604907; --  
 CC DR GO; GO:0005887; C:integral to plasma membrane; TAS.  
 CC DR GO; GO:0004872; F:receptor activity; TAS.  
 CC DR GO; GO:0007166; P:cell surface receptor linked signal transdu. . . ; TAS.  
 CC DR InterPro; IPR001368; TNFR\_C6.  
 CC DR PROSITE; PS00652; TNFR\_NGFR\_1; 1.  
 CC DR PROSITE; PS00050; TNFR\_NGFR\_2; FALSE NEG.  
 CC KW Glycoprotein; Immune response; Receptor; Repeat; Signal-anchor;  
 CC Transmembrane.  
 CC FT DOMAIN 1 165 Extracellular (Potential).  
 CC FT TRANSMEM 166 186 Signal-anchor for type III membrane  
 CC FT DOMAIN 187 293 Cytoplasmic (Potential).  
 CC FT REPEAT 33 67 TNFR-Cys 1.  
 CC FT REPEAT 70 104 TNFR-Cys 2.  
 CC FT DISULFID 34 47 By similarity.  
 CC FT DISULFID 50 62 By similarity.  
 CC FT DISULFID 54 66 By similarity.  
 CC FT DISULFID 71 86 By similarity.  
 CC FT DISULFID 89 100 By similarity.  
 CC FT DISULFID 93 104 By similarity.  
 CC FT CARBOHYD 128 128 N-linked (GlcNAc. . . ) (Potential).  
 CC FT CONFLICT 251 251 P -> L (in Ref. 2).  
 CC SQ SEQUENCE 293 AA; 31816 MW; 411799F3DE17A5EB CRC64;  
 CC  
 CC Query Match 100.0%; Score 315; DB 1; Length 293;  
 CC Best Local Similarity 100.0%; Pred. No. 9.4e-29;  
 CC Matches 62; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 CC  
 CC QY 1 ENKLRSFVNLPPELRRQRSGEVENNSDNGRYGLEHRSSEASPALPGLKLSADQALVY 60  
 CC DB 105 ENKLRSFVNLPPELRRQRSGEVENNSDNGRYGLEHRSSEASPALPGLKLSADQALVY 164  
 CC  
 CC QY 61 ST 62  
 CC DB 165 ST 166  
 CC  
 CC RESULT 3  
 CC T13X MOUSE  
 CC ID T13X MOUSE STANDARD; PRT; 249 AA.  
 CC AC Q9ET35; Q9DBZ3;  
 CC DT 28-FEB-2003 (Rel. 41, Created)  
 CC DT 28-FEB-2003 (Rel. 41, Last sequence update)  
 CC DT 05-JUL-2004 (Rel. 44, Last annotation update)  
 CC DE Tumor necrosis factor receptor superfamily member 13B (Transmembrane  
 CC activator and CAML interactor).  
 CC GN Name=TNFRSF13b; Synonyms=Taci;  
 CC OS Mus musculus (Mouse).  
 CC OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 CC OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
 CC OX NCBI\_TaxID=10090;  
 CC RN [1]  
 CC RP SEQUENCE FROM N.A.  
 CC RC TISSUE=Spleen;  
 CC RX MEDLINE=21177254; PubMed=10881172; DOI=10.1038/76889;  
 CC RA Yan M., Marsters S.A., Grewal I.S., Wang H., Ashkenazi A., Dixit V.M.;  
 CC "Identification of a receptor for BlyS demonstrates a crucial role in  
 CC humoral immunity";  
 CC RT Nat. Immunol. 1:37-41(2000).  
 CC RL [2]  
 CC RN SEQUENCE FROM N.A.  
 CC RC STRAIN=C57BL/6J; TISSUE=Lung;  
 CC RX MEDLINE=22354683; PubMed=12466851; DOI=10.1038/nature01266;



RA Okazaki Y., Furuno M., Kasukawa T., Adachi J., Bono H., Kondo S.,  
RA Nikaido I., Oseato N., Saito R., Suzuki H., Yamanaka I., Kiyosawa H.,  
RA Yagi K., Tomaru Y., Hasegawa Y., Nogami A., Schonbach C., Gojobori T.,  
RA Baldarelli R., Hill D.P., Bult C., Hume D.A., Quackenbush J.,  
RA Schriml L.M., Kanapin A., Matsuda H., Batalov S., Beisel K.W.,  
RA Blake J.A., Bradt D., Brusic V., Chothia C., Corbani L.E., Cousins S.,  
RA Dalla E., Dragani T.A., Fletcher C.F., Forrest A., Frazer K.S.,  
RA Gaasterland T., Gariboldi M., Gissi C., Godzik A., Gough J.,  
RA Grimmond S., Gustincich S., Hirokawa N., Jackson I.J., Jarvis E.D.,  
RA Kanai A., Kawaji H., Kawasawa Y., Kedzierski R.M., King B.L.,  
RA Konagaya A., Kurochkin I.V., Lee Y., Lenhard B., Lyons P.A.,  
RA Maglott D.R., Maltais L., Marchionni L., McKenzie L., Miki H.,  
RA Nagashima T., Numata K., Okido T., Pavan W.J., Perlee G., Pesole G.,  
RA Petrovsky N., Pillai R., Pontius J.U., Qi D., Ramachandran S.,  
RA Ravasi T., Reed J.C., Reed D.J., Reid J., Ring B.Z., Ringwald M.,  
RA Sandelin A., Schneider C., Semple C.A., Setou M., Shimada K.,  
RA Sultana R., Takenaka Y., Taylor M.S., Teasdale R.D., Tomita M.,  
RA Verardo R., Wagner L., Wahlestedt C., Wang Y., Watanabe Y., Wells C.,  
RA Wilming L.G., Wymshaw-Boris A., Yanagisawa M., Yang I., Yang L.,  
RA Yuan Z., Zavoian M., Zhu Y., Zimmer A., Carninci P., Hayatsu N.,  
RA Hirozane-Kishikawa T., Konno H., Nakamura M., Sakazume N., Sato K.,  
RA Shiraki T., Waki K., Kawai J., Aizawa K., Arakawa T., Fukuda S.,  
RA Hara A., Hashizume M., Imotani K., Ishii Y., Itoh M., Kagawa I.,  
RA Miyazaki A., Sakai K., Sasaki D., Shibata K., Shingawa R.,  
RA Yasunishi A., Yoshino M., Waterston R., Lander E.S., Rogers J.,  
RA Birney E., Hayashizaki Y.,  
RT "Analysis of the mouse transcriptome based on functional annotation of  
RT 60,770 full-length cDNAs.";  
RL Nature 420:563-573 (2002).  
RN [3]  
RP FUNCTION.  
RX MEDLINE=20341628; PubMed=1080535;  
RA Xia X.-Z., Treanor J., Senaldi G., Khare S.D., Boone T., Kelley M.,  
RA Theill L.E., Colombero A., Solovyev I., Lee P., McCabe S., Elliott R.,  
RA Miner K., Hawkins N., Guo J., Stolina M., Yu G., Wang J., Delaney J.,  
RA Meng S.-Y., Boyle W.J., Hsu H.,  
RT "TAC1 is a TRAF-interacting receptor for TALL-1, a tumor necrosis  
RT factor family member involved in B cell regulation.";  
RL J. Exp. Med. 192:137-143 (2000).  
RN [4]  
RP FUNCTION.  
RX MEDLINE=21322748; PubMed=11429548; DOI=10.1038/99782;  
RA Wang H., Marsters S.A., Baker T., Chan B., Lee W.P., Fu L., Tumas D.,  
RA Yan M., Dixit V.M., Ashkenazi A., Grewal I.S.,  
RT "TAC1-ligand interactions are required for T cell activation and  
RT collagen-induced arthritis in mice.";  
RL Nat. Immunol. 2:632-637 (2001).  
CC -!- FUNCTION: Receptor for TNFSF13/APRIL and TNFSF13B/TALL1/BAFF/BLYS  
CC that binds both ligands with similar high affinity. Mediates  
CC calcineurin-dependent activation of NF-AT, as well as activation  
CC of NF-kappa-B and AP-1. Involved in the stimulation of B- and T-  
CC cell function and the regulation of humoral immunity (By  
CC similarity).  
CC -!- SUBUNIT: Binds TRAF2, TRAF5 and TRAF6. Binds the NH2-terminal  
CC domain of CARD6 with its C-terminus (By similarity).  
CC -!- SUBCELLULAR LOCATION: Type III membrane protein (Probable).  
CC -!- SIMILARITY: Contains 2 TNFR-Cys repeats.  
CC -----  
CC This SWISS-PROT entry is copyright. It is produced through a collaboration  
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -  
CC the European Bioinformatics Institute. There are no restrictions on its  
CC use by non-profit institutions as long as its content is in no way  
CC modified and this statement is not removed. Usage by and for commercial  
CC entities requires a license agreement (See <http://www.isb-sib.ch/announce/>  
CC or send an email to [license@isb-sib.ch](mailto:license@isb-sib.ch)).  
CC -----  
DR EMBL; AF257673; AAC00081.1; -;  
DR EMBL; AK004668; BAB23457.1; -;  
DR MGD; MGI:1889411; Tnfrsf13b.  
DR GO; GO:0005887; C:integral to plasma membrane; IDA.  
DR GO; GO:0005031; F:tumor necrosis factor receptor activity; IDA.  
DR InterPro; IPR001368; TNFR\_c6.  
DR PROSITE; PS00652; TNFR\_NGFR\_1; FALSE\_NEG.

DR PROSITE; PS50050; TNFR\_NGFR\_2; FALSE\_NEG.  
KW Immune response; Receptor; Repeat; Signal-anchor; Transmembrane.  
FT DOMAIN 1 128 Extracellular (Potential).  
FT TRANSMEM 129 149 Signal-anchor for type III membrane  
FT protein (Potential).  
FT DOMAIN 150 249 Cytoplasmic (Potential).  
FT REPEAT 5 38 TNFR-Cys 1.  
FT REPEAT 42 76 TNFR-Cys 2.  
FT DISULFID 6 19 By similarity.  
FT DISULFID 22 34 By similarity.  
FT DISULFID 26 38 By similarity.  
FT DISULFID 43 58 By similarity.  
FT DISULFID 61 72 By similarity.  
FT DISULFID 65 76 By similarity.  
FT CONFLICT 137 137 I -> F (in Ref. 2).  
SQ SEQUENCE 249 AA; 26947 MW; CB2F2D61C2931D81 CRC64;  
  
Query Match 44.9%; Score 141.5; DB 1; Length 249;  
Best Local Similarity 53.2%; Pred. No. 2.4e-08;  
Matches 33; Conservative 7; Mismatches 13; Indels 9; Gaps 2;  
  
QY 1 ENKLSPVNLPPELRRQRSGEVNNSGRVQGLEHGRSEASPALPGLKLSADQVALVY 60  
Db 77 EKRPSSQANLQPELGPQAGEVEVRSDNSGRHQSGHG-----PGLRLSSDQTLT-Y 127  
  
QY 61 ST 62  
Db 128 CT 129  
  
RESULT 4  
Q9N146 PRELIMINARY; PRT; 156 AA.  
AC Q9N146;  
DT 01-OCT-2000 (TRENBLrel. 15, Created)  
DT 01-OCT-2000 (TRENBLrel. 15, Last sequence update)  
DT 01-OCT-2000 (TRENBLrel. 15, Last annotation update)  
DE Transmembrane activator (Fragment).  
GN Name=NF-AT;  
OS Macaca mulatta (Rhesus macaque).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Primates; Catarrhini; Cercopitheciidae;  
OC Cercopitheciinae; Macaca.  
OX NCBI TaxID=9544;  
RN [1] -;  
RP SEQUENCE FROM N.A.  
RA Arredondo J.;  
RL Submitted (JAN-2000) to the EMBL/GenBank/DBJ databases.  
DR EMBL; AF227558; AAF73400.1; -;  
DR GO; GO:0016021; C:integral to membrane; IEA.  
KW Transmembrane.  
FT NON\_TER 1  
SQ SEQUENCE 156 AA; 16170 MW; 8AD74E4D17D511D0 CRC64;  
  
Query Match 44.4%; Score 140; DB 2; Length 156;  
Best Local Similarity 96.6%; Pred. No. 2e-08;  
Matches 28; Conservative 1; Mismatches 0; Indels 0; Gaps 0;  
  
QY 34 GLEHGRSEASPALPGLKLSADQVALVYST 62  
Db 1 GLEHGRSEASPALPGLKLSADQVALVYST 29  
  
RESULT 5  
Q9VH96 PRELIMINARY; PRT; 702 AA.  
AC Q9VH96;  
DT 01-MAY-2000 (TRENBLrel. 13, Created)  
DT 01-MAY-2000 (TRENBLrel. 13, Last sequence update)  
DT 05-JUL-2004 (TRENBLrel. 27, Last annotation update)  
DE CG8358-PA (GH26575p).  
OS ORFNames=CG8358;  
OS Drosophila melanogaster (Fruit fly).

OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;  
OC Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;  
OC Ephydroidea; Drosophilidae; Drosophila.  
OX NCBI\_TaxID=7227;  
RN [1]  
RN SEQUENCE FROM N.A.  
RP MEDLINE=20196006; PubMed=10731132;  
RX Adams M.D., Ceiniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,  
RA Amanatides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galle R.F.,  
RA George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,  
RA Sutton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X.,  
RA Brandon R.C., Rogers Y.H., Blazek R.G., Champe M., Pfeiffer B.D.,  
RA Wan K.H., Doyle C., Baxter E.G., Helt G., Nelson C.R., Gabor G.L.,  
RA Abril J.F., Agbayani A., An H.J., Andrews-Pfannkoch C., Baldwin D.,  
RA Ballew R.M., Baau A., Baxendale J., Bayraktaroglu L., Beasley E.M.,  
RA Beeson K.Y., Benos P.V., Berman B.P., Bhandari D., Bolshakov S.,  
RA Borkova D., Botchan M.R., Boutck J., Brockstein P., Brotter P.,  
RA Burtis K.C., Busam D.A., Butler H., Cadieu E., Center A., Chandra I.,  
RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,  
RA de Pablos B., Delcher A., Deng Z., Mays A.D., Dew I., Dietz S.M.,  
RA Dodson K.J., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,  
RA Durbin K.J., Evangelista C.C., Ferraz C., Ferreira S., Fleischmann W.,  
RA Foesler C., Gabriellian A.E., Garg N.S., Gelbart W.M., Glasner K.,  
RA Glodek A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M.,  
RA Harris N.L., Harvey D., Heiman T.J., Hernandez J.R., Houck J.,  
RA Hostin D., Houston K.A., Howland T.J., Wei M.H., Ibegwam C.,  
RA Jalali M., Kalush F., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A.,  
RA Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z.,  
RA Lasko P., Lei Y., Levitsky A.A., Li J., Li Z., Liang Y., Lin X.,  
RA Liu X., Mattei B., McIntosh T.C., McLeod M.P., McPherson D.,  
RA Merkulov G., Milshina N.V., Mobarry C., Morris J., Moshrefi A.,  
RA Mount S.M., Moy M., Murphy B., Murphy L., Muzny D.M., Nelson D.L.,  
RA Nelson D.R., Nelson K.A., Nixon K., Nusskern D.R., Pacleb J.M.,  
RA Palazzolo M., Pittman G.S., Pan K., Pollard J., Puri V., Reese M.G.,  
RA Reinert K., Remington K., Saunders R.D., Scheeler F., Shen H.,  
RA Shue B.C., Siden-Kiamos I., Simpson M., Skupski M.P., Smith T.,  
RA Spier E., Spradling A.C., Stapleton M., Strong R., Sun E.,  
RA Svirskaas R., Tector C., Turner R., Venter E., Wang A.H., Wang X.,  
RA Wang Z.Y., Wassarman D.A., Weinstein G.M., Weissbach J.,  
RA Williams S.M., Woodgett J., Worley K.C., Wu D., Yang S., Yao Q.A., Ye J.,  
RA Yeh R.F., Zaveri J.S., Zhan M., Zhang G., Zhao Q., Zhu X.,  
RA Zheng X.H., Zhong F.N., Zhong W., Zhou X., Zhu S., Smith H.O.,  
RA Gibbs R.A., Myers E.W., Rubin G.M., Venter J.C.;  
RT "The genome sequence of Drosophila melanogaster";  
RT Science 287:2185-2195(2000).  
RN [2]  
RN SEQUENCE FROM N.A.  
RP MEDLINE=22426065; PubMed=12537568;  
RX Ceiniker S.E., Wheeler D.A., Kronmiller B., Carlson J.W., Halpern A.,  
RA Patel S., Adams M., Champe M., Dugan S.P., Frise E., Hodgson A.,  
RA George R.A., Hoskins R.A., Laverty T., Muzny D.M., Nelson C.R.,  
RA Pacleb J.M., Park S., Pfeiffer B.D., Richards S., Sodergren E.J.,  
RA Weinstock G., Scherer S.E., Myers E.W., Gibbs R.A., Rubin G.M.;  
RT "Finishing a whole-genome shotgun: release 3 of the Drosophila  
melanogaster euchromatic genome sequence";  
RT Genome Biol. 3:RESEARCH0079-RESEARCH0079(2002).  
RN [3]  
RN SEQUENCE FROM N.A.  
RP MEDLINE=22426070; PubMed=12537573;  
RX Kaminker J.S., Bergman C.M., Kronmiller B., Carlson J., Svirskaas R.,  
RA Patel S., Frise E., Wheeler D.A., Lewis S.E., Rubin G.M.,  
RA Ashburner M., Ceiniker S.E.;  
RT "The transposable elements of the Drosophila melanogaster euchromatin:  
a genomics perspective";  
RT Genome Biol. 3:RESEARCH0084-RESEARCH0084(2002).  
RN [4]  
RN SEQUENCE FROM N.A.  
RP MEDLINE=22426069; PubMed=12537572;  
RX Milra S., Crosby M.A., Mungall C.J., Matthews B.B., Campbell K.S.,  
RA Hradecky P., Huang Y., Kaminker J.S., Millburn G.H., Prochnik S.E.,  
RA Smith C.D., Tupy J.L., Whitfield E.J., Bayraktaroglu L., Berman B.P.,  
RA Bettencourt B.R., Ceiniker S.E., de Grey A.D., Drysdale R.A.,

DR CO; GO:0006355; P:regulation of transcription, DNA-dependent; IEA.  
DR InterPro; IPR001356; LIM domain; Metal-binding; Nuclear protein;  
DR InterPro; IPR001781; LIM.  
DR InterPro; IPR007107; LIM homeo.  
DR Pfam; PF00046; Homeobox; 1.  
DR Pfam; PF00412; LIM; 2.  
DR ProDom; PD000010; Homeobox; 1.  
DR ProDom; PD000094; LIM; 2.  
DR SMART; SM00389; HOX; 1.  
DR SMART; SM00132; LIM; 2.  
DR PROSITE; PS00027; HOMEBOX 1; 1.  
DR PROSITE; PS00071; HOMEBOX 2; 1.  
DR PROSITE; PS00478; LIM DOMAIN 1; 2.  
DR PROSITE; PS00023; LIM DOMAIN 2; 2.  
KW DNA-binding; Homeobox; LIM domain; Metal-binding; Nuclear protein;  
KW Zinc.  
SQ SEQUENCE 480 AA; 53720 MW; DB884B7CA0F5A575 CRC64;  
Query Match 21.0%; Score 66; DB 2; Length 480;  
Best Local Similarity 30.4%; Pred. No. 43;  
Matches 14; Conservative 10; Mismatches 18; Indels 4; Gaps 1;  
QY 6 SPVNLPELRQRSGEV-----ENNDSNGRYGLEHRSSEASPALP 47  
DB 181 TPATTPDDLDRVKDASIMNNNNNNNNNNHREAGLENRENTAGIP 226  
RESULT 7  
Q9GUY6 PRELIMINARY; PRT; 480 AA.  
AC Q9GUY6  
DT 01-WAR-2001 (TREMELREL. 16, Created)  
DT 01-WAR-2001 (TREMELREL. 16, Last sequence update)  
DT 01-WAR-2004 (TREMELREL. 26, Last annotation update)  
DE Transcription factor Hplim1.  
GN Name=Hplim1;  
OS Hemictrotus pulcherrimus (Sea urchin).  
OC Eukaryota; Metazoa; Echinodermata; Eleutherozoa; Echinozoa;  
OC Echinoidea; Echinozoa; Echinacea; Echinozoa; Strongylocentrotidae;  
OC Hemictrotus.  
OC NCBI\_TaxID=7650;  
OX [1]  
RN [1]  
RP SEQUENCE FROM N.A.  
RX MEDLINE=99325976; PubMed=10400389;  
RA Kawasaki T., Mitsunaga-Nakatsubo K., Takeda K., Akasaka K.,  
RA Shinada H.;  
RT "Lim1 related homeobox gene (Hplim1) expressed in sea urchin  
embryos.";  
RL Dev. Growth Differ. 41:273-282(1999).  
RN [2]  
RP SEQUENCE FROM N.A.  
RA Kawasaki T., Mitsunaga-Nakatsubo K., Takeda K., Akasaka K.,  
RA Shinada H.;  
RL Submitted (SEP-2000) to the EMBL/GenBank/DBJ databases.  
CC -!- SUBCELLULAR LOCATION: Nuclear (By similarity).  
CC -!- SIMILARITY: Contains 2 LIM zinc-binding domains.  
DR EMBL; AB049118; BAB13725.1; -.  
DR HSP; P06601; 1FJL.  
DR GO; GO:0005634; Cnucleus; IEA.  
DR GO; GO:0003700; F:transcription factor activity; IEA.  
DR GO; GO:0008270; F:zinc ion binding; IEA.  
DR GO; GO:0006355; P:regulation of transcription, DNA-dependent; IEA.  
DR InterPro; IPR001356; Homeobox.  
DR InterPro; IPR009057; Homeodomain\_like.  
DR InterPro; IPR001781; LIM.  
DR InterPro; IPR007107; LIM homeo.  
DR Pfam; PF00046; Homeobox; 1.  
DR Pfam; PF00412; LIM; 2.  
DR PRINTS; PR00024; HOMEBOX.  
DR SMART; SM00389; HOX; 1.  
DR SMART; SM00132; LIM; 2.  
DR PROSITE; PS00027; HOMEBOX 1; 1.  
DR PROSITE; PS00071; HOMEBOX 2; 1.

DR PROSITE; PS00478; LIM DOMAIN 1; 2.  
DR PROSITE; PS00023; LIM DOMAIN 2; 2.  
KW DNA-binding; Homeobox; LIM domain; Metal-binding; Nuclear protein;  
KW Zinc.  
SQ SEQUENCE 480 AA; 53636 MW; EDCBCCBEC841A5D6 CRC64;  
Query Match 21.0%; Score 66; DB 2; Length 480;  
Best Local Similarity 30.4%; Pred. No. 43;  
Matches 14; Conservative 10; Mismatches 18; Indels 4; Gaps 1;  
QY 6 SPVNLPELRQRSGEV-----ENNDSNGRYGLEHRSSEASPALP 47  
DB 181 TPATTPDDLDRVKDASIMNNNNNNNNNNHREAGLENRENTAGIP 226  
RESULT 8  
Q942X2 PRELIMINARY; PRT; 497 AA.  
AC Q942X2  
DT 01-DEC-2001 (TREMELREL. 19, Created)  
DT 01-DEC-2001 (TREMELREL. 19, Last sequence update)  
DT 01-OCT-2003 (TREMELREL. 25, Last annotation update)  
DE Putative serine/threonine kinase PBS1 protein.  
GN Name=P0492609.25;  
OS Oryza sativa (japonica cultivar-group).  
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;  
OC Ehrhartoideae; Oryzaceae; Oryza.  
OX NCBI\_TaxID=39947;  
RN [1]  
RP SEQUENCE FROM N.A.  
RA Sasaki T., Matsumoto T., Yamamoto K., Sakata K., Baba T., Katayose Y.,  
RA Wu J., Niimura Y., Cheng Z., Nagamura Y., Antonio B.A., Kanamori H.,  
RA Hosokawa S., Masukawa M., Arikawa K., Chiden Y., Hayashi M.,  
RA Okamoto M., Ando T., Aoki H., Arica K., Hamada M., Harada C.,  
RA Hijishita S., Honda M., Ichikawa Y., Idonuma A., Iijima M., Ikeda M.,  
RA Ikono M., Itoh S., Itoh T., Itoh Y., Iwabuchi A., Kamiya K.,  
RA Karasawa W., Katagiri S., Kikuta A., Kobayashi N., Kono I.,  
RA Machita K., Maehara T., Mizuno H., Mizubayashi T., Mukai Y.,  
RA Nagasaki H., Nakashima M., Nakama Y., Nakamichi Y., Nakamura M.,  
RA Namiki N., Negishi M., Ohta I., Ono N., Saji S., Sakai, K., Shibata M.,  
RA Shimokawa T., Shomura A., Song J., Takazaki Y., Terasawa K., Tsuji K.,  
RA Waki K., Yamagata H., Yamane H., Yoshiki S., Yoshihara R., Yukawa K.,  
RA Zhong H., Iwama H., Endo T., Ito H., Hahn J.H., Kim H.I., Eun M.Y.,  
RA Yano M., Jiang J., Gojobori T.;  
RT "The genome sequence and structure of rice chromosome 1.";  
RL Nature 420:312-316(2002).  
CC -!- SIMILARITY: Belongs to the Ser/Thr protein kinase family.  
DR EMBL; AF003266; BAB4203.1; -.  
DR Gramene; Q942X2; -.  
DR GO; GO:0005524; F:ATP binding; IEA.  
DR GO; GO:0004674; F:protein serine/threonine kinase activity; IEA.  
DR GO; GO:0006468; F:protein amino acid phosphorylation; IEA.  
DR InterPro; IPR011009; Kinase like.  
DR InterPro; IPR000719; Prot kinase.  
DR InterPro; IPR008271; Ser thr\_pkin\_AS.  
DR Pfam; PF00069; Pkinase; 1.  
DR ProDom; PD000001; Prot kinase; 1.  
DR PROSITE; PS00107; PROTEIN\_KINASE\_ATP; 1.  
DR PROSITE; PS00111; PROTEIN\_KINASE\_DOM; 1.  
DR PROSITE; PS00108; PROTEIN\_KINASE\_ST; 1.  
KW ATP-binding; Kinase; Serine/threonine-protein kinase; Transferase.  
SQ SEQUENCE 497 AA; 54925 MW; 6DB0C1FAPDE0213E CRC64;  
Query Match 21.0%; Score 66; DB 2; Length 497;  
Best Local Similarity 35.9%; Pred. No. 44;  
Matches 23; Conservative 11; Mismatches 20; Indels 10; Gaps 4;  
QY 4 LRSPVNLPELRQRSGEV-----NNSDSNGRYQGLEH---RGSE-ASPALPKLSA 53  
DB 401 VRSPNHSPDLRREARRSRAEVSRTSGDSGRSGRLDLDMTGSGSPAQTKRKRET 460  
QY 54 DQVA 57

|    |   |
|----|---|
| RC | STRAIN=SARG / COMP 1375 / SS120;  |
| RX | MEDLINE=22810154; PubMed=12917486;  |
| RA | Dufrene A., Salanoud M., Partensky F., Artiguenave F., Axmann I.M.,       |
| RA | Barbe V., Duprat S., Galperin M.Y., Koonin E.V., Le Gall F.,              |
| RA | MAkarova K.S., Ostrowski M., Oztas S., Robert C., Rogozin I.B.,           |
| RA | Scanlan D.J., Tandeau de Marsac N., Weissenbach J., Wincker P.,           |
| RA | Wolf Y.I., Hess W.R.;   |
| RT | "Genome sequence of the cyanobacterium Prochlorococcus marinus SS120,     |
| RT | a nearly minimal oxyphototrophic genome."                                 |
| RL | Proc. Natl. Acad. Sci. U.S.A. 100:10020-10025(2003).                      |
| DR | EMBL; AE017163; AAP99987.1; --  |
| DR | GO; GO:0008686; F:3.4 dihydroxy-2-butanone-4-phosphate syntha. . . ; IEA. |
| DR | GO; GO:0003935; F:GTP cyclohydrolase II activity; IEA.                    |
| DR | GO; GO:0009331; P:vitamin B2 biosynthesis; IEA.                           |
| DR | InterPro; IPRO00422; DHBP synthase.                                       |
| DR | InterPro; IPRO00926; GTP cyclohydroII.                                    |
| DR | Pfam; PF00926; DHBP synthase; 1.  |
| DR | Pfam; PF00925; GTP Cyclohydro2; 1.  |
| DR | ProDom; PD003034; DHBP synthase; 1.                                       |
| DR | TIGRFAMS; TIGR00505; rbaA; 1.   |
| DR | TIGRFAMS; TIGR00506; ribB; 1.   |
| KW | Complete proteome.  |
| SQ | SEQUENCE 546 AA; 60348 MW; 05453CE83073B5FE CRC64;                        |

  

|                          |                                      |
|--------------------------|--------------------------------------|
| Query Match              | 21.0%; Score 66; DB 2; Length 546;   |
| Best Local Similarity    | 27.9%; Pred. No. 50;                 |
| Matches 17; Conservative | 12; Mismatches 24; Indels 8; Gaps 1; |

  

|    |  |
|----|--|
| Qy | 5 RSPVNLPP-----ELRRQRSGEVENNDSNGRYQGLEHGRGSASPALPKGLKSADQV 56    |
| Db | 382 REPLVINPTDYNNYLAIRKTLGHYIGNDDSDGKYVIYWKGVSSNMLSAYKNKAQEI 441 |
| Qy | 57 A 57  |
| Db | 442 A 442  |

  

|                   |  |
|-------------------|--|
| RESULT 11         |  |
| Q9JHT9            | ID Q9JHT9 PRELIMINARY; PRT; 554 AA.                                  |
| AC                | Q9JHT9;  |
| DT                | 01-OCT-2000 (TrEMBLrel. 15, Created)                                 |
| DT                | 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)                    |
| DE                | 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)                  |
| DE                | Guanine nucleotide exchange factor.                                  |
| GN                | Name=Ngef; Synonyms=gef;   |
| OS                | Mus musculus (Mouse).  |
| OC                | Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;    |
| OC                | Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.   |
| NCBI_TaxID=10090; | [1]  |
| RP                | SEQUENCE FROM N.A.   |
| RP                | TISSUE=Brain;  |
| RC                | MEDLINE=20241931; PubMed=10777665;                                   |
| RX                | Rodrigues N.R., Theodosiou A.M., Nesbit M.A., Campbell L.,           |
| RX                | Tandil A.T., Saranath D., Davies K.E.;                               |
| RT                | "Characterization of Ngef, a novel member of the DbI family of genes |
| RT                | expressed predominantly in the caudate nucleus.";                    |
| RL                | Genomics 65:53-61(2000).   |
| DR                | EMBL; AJ238998; CAC00698.1; --                                       |
| DR                | HSSP; O08839; lBB9.  |
| DR                | MGD; MG1:1858414; Ngef.  |
| DR                | GO; GO:0008151; P:cell growth and/or maintenance; IDA.               |
| DR                | InterPro; IPRO01849; PH.   |
| DR                | InterPro; IPRO11036; PH related.                                     |
| DR                | InterPro; IPRO00219; RhGEF.  |
| DR                | InterPro; IPRO01452; SH3.  |
| DR                | Pfam; PF00169; PH; 1.  |
| DR                | Pfam; PF00621; RhGEF; 1.   |
| DR                | Pfam; PF00018; SH3 1; 1.   |
| DR                | ProDom; PD000066; SH3; 1.  |
| DR                | SMART; SM00233; PH; 1.   |
| DR                | SMART; SM00325; RhGEF; 1.  |

DR SMART; SM00326; SH3; 1.  
DR PROSITE; PS50010; DH\_2; 1.  
DR PROSITE; PS50003; PH DOMAIN; 1.  
DR PROSITE; PS50002; SH3; 1.  
KW SH3 domain.  
SQ SEQUENCE 554 AA; 64837 MW; 5F3A8FAFBFF5914 CRC64;  
Query Match 21.0%; Score 66; DB 2; Length 554;  
Best Local Similarity 32.1%; Pred. No. 51;  
Matches 17; Conservative 8; Mismatches 22; Indels 6; Gaps 1;  
QY 13 ELRRQSGEVENNSDNS-----GRYQGLEHRSSEASPALPGLKLSADOVALV 59  
Db 34 ETRQQDAIQNSDGSQVGEDAGEEEEEEEELASPPERRALPOICLL 86  
RESULT 12  
Q923H2 ID Q923H2 PRELIMINARY; PRT; 620 AA.  
AC Q923H2;  
DT 01-DEC-2001 (TReMBLrel. 19, Created)  
DT 01-DEC-2001 (TReMBLrel. 19, Last sequence update)  
DT 01-OCT-2003 (TReMBLrel. 25, Last annotation update)  
DE Ephexin.  
GN Name=Ngef;  
OS Mus musculus (Mouse).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
OX NCBI\_TaxID=10090;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN=C57BL/6;  
RX MEDLINE=21234975; PubMed=11336673;  
RA Shanah S.M., Lin M.Z., Goldberg J.L., Estrach S., Sahlin M., Hu L.,  
RA Bazalakova M., Neve R., Corfas G., Debant A., Greenberg M.E.;  
RT "Epha receptors regulate growth cone dynamics through the novel  
guanine nucleotide exchange factor ephexin.";  
RL Cell 105:233-244(2001).  
DR EMBL; AY038025; AAK71494.1; --  
DR HSSP; O08839; 1BB9.  
DR MGD; MGI:1858414; Ngef.  
DR GO; GO:0008151; P:cell growth and/or maintenance; IDA.  
DR InterPro; IPR001849; PH.  
DR InterPro; IPR011036; PH related.  
DR InterPro; IPR000219; RhGEF.  
DR InterPro; IPR001452; SH3.  
DR Pfam; PF00169; PH; 1.  
DR Pfam; PF00621; RhGEF; 1.  
DR Pfam; PF00018; SH3; 1.  
DR ProDom; PD000066; SH3; 1.  
DR SMART; SM00233; PH; 1.  
DR SMART; SM00325; RhGEF; 1.  
DR SMART; SM00326; SH3; 1.  
DR PROSITE; PS50010; DH\_2; 1.  
DR PROSITE; PS50003; PH DOMAIN; 1.  
DR PROSITE; PS50002; SH3; 1.  
KW SH3 domain.  
SQ SEQUENCE 620 AA; 71445 MW; C2C3A9C1B6F78402 CRC64;  
Query Match 21.0%; Score 66; DB 2; Length 620;  
Best Local Similarity 32.1%; Pred. No. 58;  
Matches 17; Conservative 8; Mismatches 22; Indels 6; Gaps 1;  
QY 13 ELRRQSGEVENNSDNS-----GRYQGLEHRSSEASPALPGLKLSADOVALV 59  
Db 100 ETRQQDAIQNSDGSQVGEDAGEEEEEEEELASPPERRALPOICLL 152  
RESULT 13  
Q8CHT1 ID Q8CHT1 PRELIMINARY; PRT; 710 AA.  
AC Q8CHT1;  
DT 01-MAR-2003 (TReMBLrel. 23, Created)

DT 01-MAR-2003 (TReMBLrel. 23, Last sequence update)  
DT 01-OCT-2003 (TReMBLrel. 25, Last annotation update)  
DE Ngef protein.  
GN Name=Ngef;  
OS Mus musculus (Mouse).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
OX NCBI\_TaxID=10090;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN=FVB/N; TISSUE=Kidney;  
RX MEDLINE=2388257; PubMed=12477932;  
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,  
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,  
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,  
RA Hopkins R.P., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,  
RA Diatchenko L., Marusina K., Farmer A., Rubin G.M., Hong L.,  
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,  
RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,  
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,  
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,  
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,  
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,  
RA Fahey J., Helton E., Kettman M., Madan A., Rodrigues S., Sanchez A.,  
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,  
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,  
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,  
RA Krzywinski M.I., Skalska U., Smallos D.E., Schnerch A., Schein J.E.,  
RA Jones S.J., Marra M.A.;  
RT "Generation and initial analysis of more than 15,000 full-length human  
and mouse cDNA sequences.";  
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).  
RN [2]  
RP SEQUENCE FROM N.A.  
RC STRAIN=FVB/N; TISSUE=Kidney;  
RX Strausberg R.;  
RL Submitted (NOV-2002) to the EMBL/GenBank/DBJ databases.  
DR EMBL; BC039279; AAH39279.1; --  
DR HSSP; O08839; 1BB9.  
DR MGD; MGI:1858414; Ngef.  
DR GO; GO:0008151; P:cell growth and/or maintenance; IDA.  
DR InterPro; IPR001849; PH.  
DR InterPro; IPR011036; PH related.  
DR InterPro; IPR000219; RhGEF.  
DR InterPro; IPR001452; SH3.  
DR Pfam; PF00169; PH; 1.  
DR Pfam; PF00621; RhGEF; 1.  
DR Pfam; PF00018; SH3; 1.  
DR ProDom; PD000066; SH3; 1.  
DR SMART; SM00233; PH; 1.  
DR SMART; SM00325; RhGEF; 1.  
DR SMART; SM00326; SH3; 1.  
DR PROSITE; PS50010; DH\_2; 1.  
DR PROSITE; PS50003; PH DOMAIN; 1.  
DR PROSITE; PS50002; SH3; 1.  
KW SH3 domain.  
SQ SEQUENCE 710 AA; 82198 MW; F255DE351E02A586 CRC64;  
Query Match 21.0%; Score 66; DB 2; Length 710;  
Best Local Similarity 32.1%; Pred. No. 68;  
Matches 17; Conservative 8; Mismatches 22; Indels 6; Gaps 1;  
QY 13 ELRRQSGEVENNSDNS-----GRYQGLEHRSSEASPALPGLKLSADOVALV 59  
Db 190 ETRQQDAIQNSDGSQVGEDAGEEEEEEEELASPPERRALPOICLL 242  
RESULT 14  
Q8TEJ7 ID Q8TEJ7 PRELIMINARY; PRT; 677 AA.  
AC Q8TEJ7;  
DT 01-JUN-2002 (TReMBLrel. 21, Created)  
DT 01-JUN-2002 (TReMBLrel. 21, Last sequence update)

